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OM protein - protein search, using sw model

Run on:

September 15, 2003, 17:16:01; Search time 36.7714 Seconds (without alignments) 112.231 Million cell updates/sec

138 1 NIWAAQRYGRELRRMSDEFEGSFKGL (26 US-09-544-664-1 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues

Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Bcl2 polypeptide B	Shorter murine BAD	bcl-x(L)/bcl-2 ass	Murine BCL-XL/BCL-	Mutant BCL-XL/BCL-				
QI		AAB37002	AAB37003	AAB37056	AAB37055	AAB70370	AAR95168	AAW61315	AAW61316
DB	21	21	21	21	21	22	17	19	19
Length	26	36	27	K	28	162	204	204	1204
Query Match Length DB	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Mutant BCL-XI./BCL-	t BCL-XL/	BAD	: muri	Murine BAD protein	Bad-DITR apoptosis	Human Bad peptide	PTPC-interacting T	Mutant Bc12 compet	2	щ	Bad 1		rL/Bcl	Human cell prolife	Human BAD mutant a	Human Bad protein.	Amino acid sequenc	Human BAD protein	Human ovarian anti	bcl-x(L)/bcl-2 ass	Mutant Bc12 compet	Human Bad peptide	BC	Mutant Bcl2 compet	Human Bad peptide	Human Bad peptide	Ψ.	Mutant Bc12 compet	BC	Mutant Bcl2 compet	Human Bad peptide	rrd.	Human Bad peptide	7	Human Bad peptide
1 2 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3	AAW6131	, ω	AAB7036	ABR3908	AAU0022	AAU7862	ABP5616	ABG7848	ABG7849	AAU7861	AAU7862	AAW3247	AAW5577	AAB1351	AAB7036					17 AAR95166														ABG784	AAU7861
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100	100.0	100.0	100.0	100.0	100.0	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	81.9	80.4	80.4	79.7	79.7	79.7	79.7	79.0	79.0	79.0	79.0	79.0	79.0	79.0	78.3	78.3
138	138	138	138	138	138	114	114	114	114	114	114	114	114	114	114	114	114	114	114	113	111	111	110	110	110	110	109	109	109	109	109	109	109	108	108
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## ALIGNMENTS

Bcl2 polypeptide BH3 domain peptide #1. 26 AA. AAB37001 standard; peptide; 28-FEB-2001 (first entry) AAB37001; RESULT 1 

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1.

12-OCT-2000,

06-APR-2000; 2000WO-US09352.

(UYJE-) UNIV JEFFERSON THOMAS.

99US-0128202.

07-APR-1999;

Lu Z; Huang Z, Wang J, Zhang Z, Shan S,

WPI; 2000-679325/66.

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The invention relates to a peptide conjugate having the formula:

(R.Yn-peptide where n = 1-10; X = C=0, when the R-Y group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH, when the R-Y group of the peptide, or OH; or X = 0 or NH, when the R-Y group is attached to the C-terminus of the peptide, or a side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclopentyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AB37001-39736s represent analogues of the peptide portion of the conjugate. The peptides corresponding to amino acids 72-97 of the BH3 amain of the cell death agonist Bad. The peptide corrigate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting BCl-2 cunticion. In particular, the peptide conjugate is useful for treating a subject apoptosis and an expensive an
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                       New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                        Claim 18; Page 17; 74pp; English.
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The invention relates to a peptide conjugate having the formula:

(R-X)n peptide where n = 1-10; X = C=O, when the R-X group is attached
to the N-terminus of the peptide, or a side chain of the peptide where
the functional group of the side chain is NH2 or OH; or X = O or NH,
when the R-X group is attached to the C-terminus of the peptide, or a
side chain of the peptide, where the side chain functional group is COOH
or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylpatol containing one
or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylpatol containing one
or two double bonds, cyclobutyl, cyclopentyl, cyclobaxyl optionally
monosubstituted with a 1-SC straight or branched chain
c the peptide portion of the conjugate. The peptides represent examples
of the peptide portion of the conjugate. The peptides represent analogues
of the peptide portion of the conjugate. The peptide conjugate is
useful for modulating apoptosis in the calls of a subject, or for
reversing B cell lymphoma/lenkamia 2 (BBL-2)-mediated blockage of
apoptosis in cancer cells. It is also useful for inhibiting Bol-2
unction. In particular, the peptide conjugate is useful for treating a
subject affilicted with a cancer characterized by cancer cells that
express Bol-2. The cancer characterized by cancer cells that
express Bol-2. The cancer characterized by cancer cells that
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                                                                                                                                                 New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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Zhang Z,
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    Wang J,
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached to the roll of the peptide where to the Vibramius of the peptide, or a side chain of the peptide, or a side chain of the peptide, where the side chain of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl contraining one or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl contraining one or CONH2; and R = 2-18C alkyl croppentyl, cyclopentyl, cyclopexyl optionally one mosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB7001-B37058 represent amalogues of the peptide portion of the conjugate. The peptides represent amalogues of the BH3 domain of the conjugate. The peptide conjugate is of a Bcl-2 superiamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the coll death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for eversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of unction. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that cancer includes prostate, colorectal, gastric, on-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is a conjugate is conjugate is conjugate is conjugate in cancers, neuroblastoma, melanoma, or conjugate is also useful for treating disconjugate is conjugate is a conjugate in cancers, neuroblastoma, melanoma, or conjugate is also useful for treating disconjugate is a conjugate in cancers, neuroblastoma, melanoma, or conjugate is also useful for treating disconding a provisor of the peptide conjugate is useful for treating a neuroper conjugate is useful for treating a neuroper conjugate is useful for tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                           Lu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bcl2 polypeptide BH3 domain peptide #56.
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                                                                         Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB37056 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                               Claim 18; Page 17; 74pp; English.
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                        (UYJE-) UNIV JEFFERSON THOMAS.
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                                                                                                                          WPI; 2000-679325/66.
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                                                                         Huang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the vertical group of the spetide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, or X = COX NH2.

The functional group of the side chain is NH2 or OH; or X = O or NH, or X = O or X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                       New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma, melanoma; lymphocytic leukemia; neurodegenerative disorder; AlDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                       Wang J, Zhang Z, Shan. S,
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                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB37055 standard; peptide; 28
                                                                                                     (UYJE-) UNIV JEFFERSON THOMAS.
06-APR-2000; 2000WO-US09352.
                                                    99US-0128202,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001 (first entry)
                                                                                                                                                                                                     WPI; 2000-679325/66.
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                                                    07-APR-1999;
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Best Local S
                                                                                                                                                       Huang Z,
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Mus musculus.

Synthetic.

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide where the functional group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COH CC COMES; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB7001-BB7058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the call death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 [801-2), mediated blockage of unction. In particular, the peptide conjugate is useful for treating a conserses Bcl-2. The cancer characterized by cancer cells that express Bcl-2. The cancer characterized by cancer cells that express Bcl-2. The cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, colored conjugate is also useful for treating a cute or chronic lymphocytic and non-lymphocytic and non-lymphocytic and non-lymphocytic and non-lymphocytic and conjugate is also useful for treating a conjugate is also useful for treating a colored and a conjugate is also useful for treating a colored and a conjugate is also useful for treating a colored and a conjugate is also useful for treating a colored and a conjugate is also useful for treating a colored and a col
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                                                          New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 138; DB 21;
100.0%; Pred. No. 2.1e-14;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                 Huang Z, Wang J, Zhang Z, Shan S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                          (UYJE-) UNIV JEFFERSON THOMAS.
                                                                              06-APR-2000; 2000WO-US09352.
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Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                      WPI; 2000-679325/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 AA;
                       12-OCT-2000.
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AAB70370
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The present invention describes an isolated or synthetic polypeptide

(1) comprising a less than full length amino acid sequence of a mutant

EDI-XL/BAD-12 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Serl18 of a human

BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

nootropic, antilistaemic, vulnerary, cytostatic, antiviral,
antiarthrito, antiliflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

polymuclectides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

inducing or inhibiting apoptosis in a cell. Candidate compounds

indentified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

lymphoproliferative conditions, arthritis, infertility, infamination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypebide; bcl-x; cell death; regulate; BHI; BHS; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases. The present sequence represents a specifically claimed shorter murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                             New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
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100.0%; Pred. No. 1.5e-13;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 148-149; 157pp; English.
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                                                                                                                                                                                                                                (APOP-) APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                         99US-0136783.
                                                                                                                                                   30-MAY-2000; 2000WO-US11864.
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                                                                        WO200110888-A1.
                                                                                                                                                                                         28-MAY-1999;
                                                                                                             15-FEB-2001.
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Best Local 9
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Mus musculus

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (2) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infarmation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease. Polynucleotide sequences continuants phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorylated BAD, by usual immunoassays: Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or ECL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 10; 95pp; English.
                                                                                                                                97WO-US19175
                                                                                                                                                                                              96US-0733505
                                                                                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON
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                                                                                                                                                                                                                                                                                                                               Korsmeyer SJ;
                                                                                                                                17-0CT-1997;
                                                                                                                                                                                              .8-OCT-1996;
W09817682-A1
                                                                 30-APR-1998,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates call death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L). Bad competes with Bax for binding death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to bal-2 or bal-x(L) to form heterodimers. Such agents may be treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers
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                                                                                                        /note= "BH2 conserved amino acids"
38..61
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1,9e-13;
thes 0;
                                  147..149
/note= "BH1 conserved amino acids"
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                                                                                                                                                                                    /note= "PEST sequence"
111..130
                                                                                                                                                                                                                                                             /note= "PEST sequence"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. AIDS, senescence or ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 1; 130pp; English.
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                                                                                             .192
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N-PSDB; AAT29479.
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Korsmeyer SJ;
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AAW61315
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                                                   Gaps
                                                0
     Length 204;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Mutant BCL-XL/BCL-2 associated cell death regulator #1.
100.0%; Score 138; DB 19;
100.0%; Pred. No. 1.9e-13;
ive 0; Mismatches 0;
                                                                                                                             140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                 1 NLWAAQRYGRELRRMSDEFEGSFKGL
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30-APR-1998.
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                                                                                                                                                                                                                                                                              The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 94 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that instend in the factor or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screening. BAD proteins phosphorylated at specified Ser are used to screening. BAD and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptosic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphated BAD by usual immunoassays. Mutant BAD proteins have greater death-pronotting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heteroding the service of BCL-XL but instead binds to 14-33 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins in the cytosol, thus promoting cell survival. The mutants with ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                        Claim 7; Page 59; 95pp; English.
                                        97WO-US19175.
                                                                     96US-0733505
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                                                                                                                                                       WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AA;
                                                                                                                                                                     N-PSDB; AAV27834
                                                                                                                                                                                                                             viral infection
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                                       17-0CT-1997;
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 12 and/or 186, relative to the murine BAD 204 as as equence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, Imphoproliferation, arthritis, infertility, and the gase and disease models or in fury screening. BAD proteins as disease models or in fury screening, and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischemic cell death. The apoptotic status of cells is adjugated and non-phosphorylated on the specified Ser, forming a product that does not phosphorylated cannot bind 14-3-3. Imminity cell survival. The mutants with expecting services in the cytosol, thus promoting cell survival. The mutants with
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                                                                                                                                                                                                                                                                                                                                               New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 60; 95pp; English.
97WO-US19175.
                                                            96US-0733505
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N-PSDB; AAV27835.
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                                                                                                                                                                                           Korsmeyer SJ;
17-0CT-1997;
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                                                                                                                                                Korsmeyer SJ;
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                                                                                                                                                                                                                                                                                                     death regulator) proteins, having an amino acid other than Ser at position 112 and/or 156, relative to the murine BAD 204 as sequence. The presents of mutant BAD protein. Also described are: (1) tragments of mutant BAD protein. Also described are: (1) tragments of mutant BAD with a heterologous polypeptide that conceases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infartility, infartilit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·,
                                                                                                                                                                                                                                                                                          present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                             New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 138; DB 19;
100.0%; Pred. No. 1.9e-13;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW58832 standard; protein; 204 AA
                                                                                                                                                                                                                                                             Claim 7; Page 60-61; 95pp; English.
               97WO-US19175.
                                                96US-0733505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                               (UNIW ) UNIV WASHINGTON
                                                                                                                                               WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine BAD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AA;
                                                                                                                                                              N-PSDB; AAV27836
                                                                                                                                                                                                                                viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9809643-A1.
                                                                                                                Korsmeyer SJ;
               17-0CT-1997;
                                                18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW58832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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This sequence represents a novel serine-phosphorylated protein, BAD (BCL-X1)282-12 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator.

Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased/decreased apoptors! In a cell. The increased apoptors may result from immunodeficiency diseases, senseonce, neurodegenerative disease, ischaemic cell death, repetfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; mamunosuppressive; apottosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphoproliferative condition; inflammation; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 1.9e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 8; 61pp; English.
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97WO-US15871.
                                                                                     96US-0707868
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                                                                                                                                                                     (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                       WPI; 1998-207049/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200110888-A1.
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Query Match
Best Local Similarity
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N-PSDB; ABZ81201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L6-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Region
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                  AAU00220
                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                         The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bel-XL/Bel-12 associated call death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Seril3 of a human BAD, SeriS5 of a murine BAD (longer murine BAD) or Seril3 of a murine BAD (and the acid of a mutine BAD) or seril3 of a murine BAD (and the acid of a mutine BAD) or seril3 of a murine BAD (and the acid of a mutine BAD) or seril3 of a murine BAD (and the acid of a mutine BAD) or seril3 of a murine BAD (and acid of a mutine BAD) or seril3 of a murine BAD (and acid of a mutine BAD) or series of a mutine BAD (and acid of a mutine) or inhibitions an apoptosis induced or inhibitor. BAD polypeptides are useful in treating inducing or inhibiting apoptosis in a cell. Candidate compounds indentified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell cath, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and cutolimmune diseases. The present sequence from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                            New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 138; DB 22;
100.0%; Pred. No. 1.9e-13;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR39082 standard; Protein; 204 AA.
                                                                                                                                        Claim 4; Page 148; 157pp; English.
           (APOP-) APOPIOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine BAD protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2002; 2002WO-US24177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001; 2001US-308929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 26; Conservative
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                                                      WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                 204 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
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                                 Zhou X;
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ABR39082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diptheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient isobaemic neuronal injury; stroke; spinal oord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Chimeric - Corynebacterium diptheriae
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                                                                                                                                                         Claim 15; Page 168; 192pp; English.
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Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell -
                                                                                                                                                                                                                     Claim 4; Page 59-61; 65pp; English.
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The sequence represents the amino acid sequence of Bad-DTMR apoptosismodifying fusion protein comprising Bad gene sequence fused via a short
continued apoptosis-modifying fusion protein is capable of binding a
target cell and integrating into or crossing a cellular membrane of the
carget cell and integrating into or crossing a cellular membrane of the
carget cell and integrating into or crossing a cellular membrane of the
continued apoptosis-modifying fusion protein comprises at least
two domains: the DTM domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities an apoptotic response
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continued the Bcl-XL domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities an apoptotic response
continued the Bcl-XL domain, which medities are proported as Abjective and the Bcl-XL transient ischaemic neuronal injury,
continued as Alzheimer's disease, Huntington's disease, spinal muscular
atrophy, stroke episodes and unrequiated cell growth as in tumours and
cutoptotic representative body and targeted to selective tissue and 

567 AA; Sequence

Gaps ·; Length 567; Indels Query Match 100.0%; Score 138; DB 22; Best Local Similarity 100.0%; Pred. No. 6.1e-13; Matches 26; Conservative 0; Mismatches 0;

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Search completed: September 15, 2003, 17:22:13 Job time: 37.7714 secs 161 NLWAAQRYGRELRRMSDEFEGSFKGL 186 g

1 NLWAAQRYGRELRRMSDEFEGSFKGL 26

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APP11

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                                                                                                 September 15, 2003, 17:22:21; Search time 13.5571 Seconds (without alignments) 81.144 Million cell updates/sec
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Sequence 1, Ms
Sequence 13, Ms
Sequence 13, Ms
Sequence 3, Ms
Sequence 2, Ms
Sequence 2, Ms
Sequence 1, Ms
Sequence 2, Ms
Sequence 2, Ms
Sequence 2, Ms
Sequence 2, Ms
Sequence 10, Sequence 2, Ms
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26,
34,
69,
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Sequence 2
Sequence 3
Sequence 6
Sequence 6
Sequence 6
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Sequence
                                                                                                                                                                                                                                                                                                                                         328717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/laa/5A_cOMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-333-565-2
US-08-61479-2
US-08-733-505A-12
US-08-733-505A-13
US-08-733-505A-13
US-08-733-505A-13
US-08-717-123-3
US-08-75-227-3
US-08-965-617-2
US-08-965-335-1
US-08-965-335-1
US-09-410-372-7
US-09-410-372-7
US-09-333-565-10
US-08-333-565-10
US-08-733-505A-55
US-08-733-505A-56
US-08-733-505A-56
US-08-733-505A-56
US-08-733-505A-56
US-08-733-505A-56
US-08-611-479-20
US-08-733-505A-56
US-08-611-479-20
US-08-611-479-20
US-08-611-479-20
US-08-733-505A-59
US-08-611-479-20
US-08-611-479-20
US-08-611-479-20
US-08-611-479-20
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-59
US-08-733-505A-69
US-08-733-505A-69
US-08-733-505A-69
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            138
1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                   328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %
Query
Match Length DB
                                                                                                                                                                           US-09-544-664-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                  Scoring table:
                                                                       OM protein
                                                                                                                                                                                                                  Sednence:
                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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Sequence 4656, Ap Sequence 19594, A Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 21807, A Sequence 21807, A Sequence 2, Appli Sequence 1756, A Sequence 1756, A Sequence 2775, A Sequence 27, Appli Sequence 27, Appli		
904 4 US-09-328-352-4656 610 4 US-09-328-352-4656 946 3 US-09-074-579-3 946 3 US-09-388-774-3 946 4 US-09-546-133-1 906 4 US-09-252-9918-31458 229 4 US-09-252-9918-31458 33 4 US-09-252-9918-31458 356 4 US-09-252-9918-13508 356 4 US-09-252-9918-17508 903 4 US-09-252-9918-17508 105 4 US-09-252-9918-18775 25 3 4 US-09-252-9918-18775 26 4 US-09-252-9918-18775 27 4 US-09-252-9918-18729 28 4 US-09-252-9918-18729	ALIGNMENTS	ication US/0833565 52. 52. 52. 52. 52. 52. 52. 52. 52. 52
299 299 301 300 301 301 302 302 303 303 303 303 303 303 303 303		RESULT 1 US-08-33-565-2 Sequence 2, Application US/08335 Patent No. 5622852 GENERAL INFORMATION: PAPLICANT: KORSMEYER, Stanley TITLE OF INVENTION: BC1-x/Bc1 TITLE OF INVENTION: BC2-x/Bc1 TITLE OF INVENTION: BC3-x/Bc1 STREET: 379 Lytton Avenue CITY: Palo Alto STREET: 379 Lytton Avenue CITY: Palo Alto STREET: California COUNTER: US TITLE 94301 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: PREPRIED NOTA: COMPUTER PREPAINOR DATA: APPLICATION NUMBER: 105/08/7 FILING DATE: 31-OCT-1994 CLASSIFICATION NUMBER: 105/08/7 FILING DATE: 31-OCT-1994 TELEPHONE Smith, William M REGISTRATION NUMBER: 105/08/7 TELEPHONE (415) 326-2422 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHRACTERISTICS: LENGTH: 204 amino acids TYPE: amino acids TYPE: AMINOSTICE PLOCENER TOPOLOGY: linear MOLECULE TYPE: protein
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Query Match 100.0%; Score 138; DB 1; Length 204; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 26; Conservative 0; Mismatches 0; Indels

/note= "Deduced amino acid sequence of mouse BAD."

NAME/KEY: Protein
COCATION: 1..204
OTHER INFORMATION: COTHER INFORMATION: COTHER 1800 NAME 108-333-565-2

FEATURE:

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APPLICANT: KORSKEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: SCL. XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
UNMER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 35.0
ATORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
RECISTRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETCHILL ALCALLCATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: HOWELL & HAFERKAMP, L.C. STREER: 7733 PORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
   : HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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; Sequence L2. Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 965458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,197
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TELEPHONE: (314) 727-5188
TELERAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                ST. LOUIS
: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clii.
STATE: Misc.
COUNTRY: USA
                                                                                                                                                           63105
      ADDRESSEE:
                                                                                              STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-733-505A-1
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APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SCREINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGILATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STREET: US
COUNTRY: US
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Deduced amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: P450H
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC Compatible
COMPUTER: LBM PC COMPATIBLE
COMPUTER: LBM PC COMPATIBLE
COMPUTER: LBM PC COMPATIBLE
COMPARE: Patentin Release #1.0, Version #1.25
SOTWARE: Patentin Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR PAPLICATION DATA:
FILING DATE: 31-COT-1994
ATTORNEY. AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TE
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100.0%; Score 138; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 26; Conservative 0; Mismatches 0;
                                 140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
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1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
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Patent No. 5856445
                                                                                                                                                                                                                     Sequence 2, Application US/08661479 Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
EDNGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: Protein

) LOCATION: 1.204

) OTHER INFORMATION: 

) OTHER INFORMATION: 

US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                           RESULT 2
US-08-661-479-2
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SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 5.8e-14; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FLING DATE:
CLASSIFICATION: 530
                                                                                     SSEE: HOWELL & HAPERKAMP, L.C.
17. 7733 FORSYTH BLVD., SUTTE 1400
ST. LOUIS
MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGBNT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654:
TELEPHONE: (314,727-5188
TELEPHONE: (314,727-5188
TELEPHONE: (314,727-518)
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                          NUMBER OF SEQUENCES: 6
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                   ADDRESSEE:
STREET: 77:
CITY: ST. I
STATE: MISK
                                                                                                                                                                                           63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-717-123-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: S
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                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICAMY: KORSMEYER, STANLEY J.
APPLICAMY: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                       Ouery Match 100.0%; Score 138; DB 2; Length 204; Best Local Similarity 100.0%; Pred; No. 58e-14, Matches 25; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLILOATION NUMBER: US/08/733,505A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 138; DB 2;
100.0%; Pred. No. 5.8e-14;
rative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                          1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEI/AGENT INFORMATION:
NAME: HOLLAND, DONALD. REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPONMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-733-505A-14

Sequence 14, Application US/08733505A
Patent No. SB56445
GENERAL INFORMATION:
RAPPLICANT: RORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 204 amino acids amino acids
                        LENGTH: 204 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
    SEQUENCE CHARACTERISTICS:
                                                                                   ; TOPOLOGY; linear; MOLECULE TYPE: peptide US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE: MISSU-
COUNTRY: USA
TO: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-733-505A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic TITLE OF INVENTION: Acids and Methods of Use NUMBER OF SEQUENCES: 15
OWNRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 114; DB 2; Length 168;
Pred. No. 2.6e-10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.6%; Score 114; DB 1; Length 166; 91.7%; Pred. No. 2.5e-10; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTEX: United States
LIP: 92121
COMPUTEX: United States
COMPUTEX: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-ID 1929
TELECOMMUNICATION INFORMATION:
GET PROMOBER: 13,815
REFERENCE/DOCKET NUMBER: 13,815
REPERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 NLWAAQRYGRELRRMSDEFVDSFK 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQRYGRELRRMSDEFEGSFK 24
                            NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPERENG/DOCKET NUMBER: CL-8
TELECOMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-717-123-2; Sequence 2, Application US/08717123; Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
      ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 168 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.6:
Best Local Similarity 91.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: protein US-08-717-123-2
                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-665-617-2
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CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
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GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TILLE OF INFORMATION:
GENERAL ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Galmesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HORNE, William A.
APPLICANT: HORNE, William A.
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACLES AND METHODS OF USE
FILE REFERENCE: 400140, 42891
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 1.7e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          ch 97.8%; Score 135; DB 2; Length 204; Similarity 96.2%; Pred. No. 1.7e-13; 25; Conservative 1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/665,617
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 NLWAAQRYGRELRRMTDEFEGSFKGL 165
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         P-ID 1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09375257
Patent No. 6504022
REFERENCE/DOCKET NUMBER: P-ID
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INPORATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                               TOPOLOGY: linear US-08-717-123-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.8%;
Best Local Similarity 96.2%;
Matches 25; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Mus musculus
US-09-375-257-3
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 204
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OPERATING SISTEM: DOS
SOFTWARE: FRACESO for Windows Version 2.0
CURRENT APPLICATION DAMA:
APPLICATION NUMBER: US/09/410,372
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
STREET: Palo Alto
STATE: CA
           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 NLWAAQRYGRELRRMSDEFVDSFW 126
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US-09-410-372-1
; Sequence 1, Application US/09410372
; Patent No. 6281334
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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LIBRARY: Geneu...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CLONE: 1
US-08-985-335-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                 GENERAL INCORDUST.

APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Ital, Preeti
APPLICANT: Ital, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Inst Compatible
COMPUTER: Inst Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335 |
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTLACATE:
FILING DATE:
ATTOCNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNDRER: 36,749
REPERENCE/DOCKET UNDRER: 9F-0421 US
TELECOMMUNICATION INFORMATION:
TELEPAN: 650-855-0555
TELEPAN: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TWORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Ital, Preeti
APPLICANT: Shah, Purvi
APPLICANT: COTLEY, Noil C.
TITLE OF INVENTION: PROIFFINA ASSON
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08985335 Patent No. 6080847
                                                                 ; Sequence 1, Application US/08985335; Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNORAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Watches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: SYNOI
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                             S
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                                RESULT 11
US-08-985-335-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-985-335-1
                                                                                                                                                                                                                                                                                                                                             STATE:
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APPLICANT: Tal, Pereti
APPLICANT: Sal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Ocnley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
COMPUTER: LBM COMPOTED.

OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
SOFTWARE: FastSED for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMB
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GENERAL INCORMATION:
APPLICANT: HOTHER, William A.
APPLICANT: HOTHER, William A.
TITLE OF INVENTION: ACIDS AND NETHODS OF USE
TITLE OF INVENTION: ACIDS AND NETHODS OF USE
FILE REPERBNCE: 480140,428D1
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILLIAG DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
INDER OF SEC OF THE SEC OF WINDOWS OF SEC OF WINDOWS O
                                                                                                                                                                                                          82.6%; Score 114; DB 3; Length 168; 91.7%; Pred. No. 2.6e-10; tive 0; Mismatches 2; Indels
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US-09-375-257-2
; Sequence 2, Application US/09375257
; Patent No. 6504022
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Best Local Similarity 91.7%;
Matches 22; Conservative (
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Best Local Similarity 91.7%
Matches 22; Conservative
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US-09-375-257-2
   ; TOPOLOGY: linear; IMMEDIATE SOURCE: LIBRARY: GenBank; CLONE: 1683637
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GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Tue, Henry

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purvi

APPLICANT: COLIEY, Neil C.

TITLE OF INVENTION: PROLIFERATION

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEB: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

COUNTRY: USA

CONTRY: USA
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MEDTUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
RIOR APPLICATION DATA:
APPLICATION UNMER: 08/985,335
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
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REGISTRATION NUMBER: 36,749
REFERRNCE/FOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPRONE: 650-845-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-410-372-7; Sequence 7, Application US/09410372; Patent No. 6281334
                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHRRACTERISTICS: LENGTH: 168 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
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SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-09-410-372-1
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Run on:

Sequence:

Title:

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APPLICANT: Horne, William A.

APPLICANT: Horne, William A.

PITLE ON THE CONTRONS HOUNDED BENCODING NUCLEIC TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE CURRENT APPLICATION NUMBER: US/09/922,378

CURRENT APPLICATION NUMBER: US/09/922,378

CURRENT FILING DATE: 2001-08-03

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10066179
Publication No. US20020115631A1
GEBERAL INFORMATION:
GABERAL INFORMATION:
GABLICANT: Horne, William A.
APPLICANT: OLIERGOIf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%; Score 135; DB 9; Length 20
96.2%; Pred. No. 3.3e-12;
live 1; Mismatches 0; Indels
4 US-10-008-355-8

US-09-815-242-12463

US-10-808-355-2

US-09-81-72A-23

US-09-81-72A-238

US-09-81-72A-238

US-09-34-455-162

US-09-149-045-2

US-09-149-045-2

US-09-149-045-2

US-09-149-045-2

US-10-166-357-2

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US-10-166-372-2

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US-10-166-372-2

US-09-815-242-11813

US-09-817-22-501

US-09-889-727-501

US-09-989-727-501

US-09-991-073-501

US-09-991-073-501

US-09-991-073-501

US-09-991-073-501

US-09-991-073-501

US-09-991-167-501

US-09-991-073-501
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; Sequence 3, Application US/09922378
; Patent No. US20020037869A1
; GENERAL INFORMATION:
                                                                                                                                                                  Similarity 96.2
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
  204
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US-10-066-179-3
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      Query Match
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Matches 25;
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Sequence 258, App
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                                                                                                                                        September 15, 2003, 17:25:56; Search time 20.6143 Seconds
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| Cgn2_6/ptodate/1/pubpaa/US07_ENR_PUB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US06_ENR_PUB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US08_BUB.PUB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US08_BUB.PUB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodate/1/pubpaa/US09_BUBCOMB.pep:*
| Cgn2_6/ptodate/1/pubpaa/US09_BUBCOMB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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5 US-09-26-1-258

US-09-844-657-1

US-09-844-657-7

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US-10-0844-657-7

US-10-10-179-2

US-10-10-179-2

US-10-10-276-11

US-10-238-075-1077

US-09-882-423-3

US-10-156-761-11541

US-10-156-761-11541
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1 NLWAAQRYGRELRRMSDEFEGSFKGL
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 62, Appli Sequence 198, Appl Sequence 198, Appl Sequence 13485, Apple Sequence 13485, Apple Sequence 13485, Apple Sequence 13481, Apple

Sequence 18, Appl Sequence 238, App Sequence 162, App Sequence 2, Appli

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                                                                                                     Length 168,
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Best Local Similarity 91.7%; Pred. No. 3.4e-09;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COTIEY, Neil C.
TITLE OF INVENTION: PROFIERS ASSOCIATED WITH CELL
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                  Score 114; DB 9;
Pred. No. 3.4e-09;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/410,372
FILING DATE: CUKNOWL)
ATTORNET-AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
RESERRONG-DOCKET UNBER: PF-0421 US
TELEPHONE: 650-855-0555
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US-09-894-657-1
                                                                                                                                                                                                                                                                103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                               1 NLWAAQRYGRELRRMSDEFEGSFK 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/09894657
; Patent No. US20020098569A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Dr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: single
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                                                                                                     Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative (
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Lal, Preeti
Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                ; ORGANISM: Homo sapiens
US-09-922-378-2
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US-09-894-657-1
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US-09-894-657-7
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APPLICANT: JACOTOTOT, ENTENNE DANIEL FRANCOIS
TITLE OF INVENTION: CHIMBRIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: CHIMBRIC MOLECULES CONTAINING THE APOPTOGENIC
TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: (PTFC)
FILE REPERENCE: 03495.0216
CURRENT APPLICATION NUMBER: US/10/059,261|
PRIOR FILING DATE: 2002-08-29
PRIOR PILING DATE: 2001-02-02
SOFTWARE: PARENCE AND SOFTE SOIL-02-02
SOFTWARE: PARENCE AND SORTES
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                                                                                                                                                                                                                                                                                                                                                  97.8%; Score 135; DB 14; Length 204; ilarity 96.2%; Pred. No. 3.3e-12; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Morne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
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FILE REFERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SEGTWARE: FRATSEQ for Windows Version 4.0
LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 NLWAAQRYGRELRRMTDEFEGSFKGL 165
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Sequence 258, Application US/10059261
Publication No. US20030077826A1
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-10-066-179-3
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 25; Conserv
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SEQ ID NO 2
LENGTH: 168
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US-09-922-378-2
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Best Local S
Matches 22
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TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIAL TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN FILE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN FILE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN FILE OF THE CONTEXT PRIOR PRIOR PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR PRIOR PILING DATE: 2000-04
PRIOR PRIOR PRIOR OF SEQ ID NOS: 193
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 147
LENGTH: 15
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; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
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                                                                                                       Length 168;
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                                                                                                                                                   Indels
                                                                                                  Score 114; DB 14;
Pred. No. 3.4e-09;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                      Sequence 147, Application US/10174105A Publication No. US20030068652A1 Publication No. US20030068652A1 APPLICANT: Cell Signaling Technology, Inc. APPLICANT: ZRANG, Hui APPLICANT: COMB, Michael J. APPLICANT: TAN, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9145, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HINGAL
APPLICANT: SHIRAMA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARAXI, YOSHIYUKI
                                                                                                                                                                                                                         103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFK 24
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                                                                                                     82.6%; 91.7%;
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Best Local Similarity 91.73
Matches 22; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
         ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-066-179-2
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LOCATION: (8)..(8)
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US-10-174-105A-147
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GENERAL INFORMATION:
APPLICANT: Horne, William A.; APPLICANT: Oltersdorf, Tilman
TILLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TILLE OF INVENTION: ACIDS AND METHODS OF USE; FILE REPERENCE: 480140.42801; CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
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91.7%; Pred. No. 3.4e-09;
tive 0; Mismatches 2; Indels
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Slah, Purvi
Corley, Weil C
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 50-885-0555
TELEPAX: 65-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY APPLICATION NUMBER: 09/410,372
FILING DATE: CURKNOWN>
ATTORNEY ASBRY INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 7: 0S-09-894-657-7
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Sequence 7, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Yue, Henry
Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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CLONE: 1683637
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Best Local Similarity 91.74
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-066-179-2
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LENGTH: 168
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Sequence 1077, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
PERIOD NO. US20030148324A1
GENERAL INFORMATION:
TITLE OF INVENTION: Polynuclectides which are of nature B2/D+ A- and which are isc
TITLE OF INVENTION: E.coll, and biological uses of these polynuclectides and of 1
FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-10
NUMBER OF SEQ ID NOS: 1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patterson, Chandra
IIILE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 12;
Pred. No. 1.5e+02;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPAX: 650-845-0155
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/388,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||||| :: |:: || || 610 IWAAQRNGAKVPRVRNGFTSMDIGL 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LWAAQRYGRELRRMSDEFEGSFKGL 26
                                                  APPLICANT: Hillman, Jennifer L.
                            2 LWAAQRYGRELRRMSDEFEGSF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guegler, Karl J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.1 SEQ ID NO 1077 LENGTH: 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Escherichia coli
US-10-238-075-1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.3
Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
                                                                                                                               RESULT 12
US-10-238-075-1077
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US-09-828-423-3
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                                                                                                                                                                    Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Handond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Mright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFRENCE: 50036/05002
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR APPLICATION NUMBER: US 60/274,526
NUMBER OF SEQ ID NOS: 233
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 241
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCOMMENTATION PAILID W.

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Antin C.

TITLE OF INVENTION: POLYPEPTIGES Interactive with BCL-X1
FILE REPRESENCE: 50036/05002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR PRILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 35;
                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                  36.2%; Score 50; DB 15; 56.2%; Pred. No. 12; tive 4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.1%; Score 47; DB Best Local Similarity 45.5%; Pred. No. 5; Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 241, Application US/10092750 Publication No. US20030032157A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LWAAQRYGRELRRMSDEFEGSF 23
                                                                                   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9145
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10092750 Publication No. US20030032157A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            : |: | : | | | | | : | 108 ERWGGDLRRMRDEADG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.1%;
                                                                                                                                                                                                                                                    6 ORYGRELRRMSDEFEG 21
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
                                                                                                                                                   Query Match
Best Local Similarity 56.2°
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Homo sapiens
US-10-092-750-241
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Best Local Similarity
Matches 10; Conserv
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US-10-092-750-241
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US-10-092-750-1
                                                             LENGTH:
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Search completed: September 15, 2003, 17:47:52 Job time: 21.6143 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.9%; Score 44; iDB 15; Length 272; 53.3%; Pred. No. 1.1e+02; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                            Query Match 33.3%; Score 46; DB 9; Length 946; Best Local Similarity 30.8%; Pred. No. 2.1e+02; Matches 8; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Fall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Tramenco, Robert T.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
APPLICANT: NV, H. Howard
APPLICANT: NV, H. Howard
APPLICANT: NV, H. Howard
APPLICANT: NV, H. HOWARD
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OMORA, SATOSHI
APPLICANT: OMORA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, VOSHIVKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-276089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ. ID NOS: 15109
                                                                                                                                                                                                                  CLONE: 9133985
SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 DVWVIEPOGLRFLHVPDTFEGHFDGV 237
                                                                                                                                                                                                                                                                                                                                                                                                           1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11541, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5704, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                   LENGTH: 946 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEEBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WAAQRYGRELRRMSD 17
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29 WIAAAHGAELRRAAD 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 8; Conserv
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US-10-156-761-11541
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US-09-815-242-5704
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                                                                                                                                                                                                                                                               US-09-828-423-3
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Gaps
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                                                    CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
SEQ ID NOS: 14110
SEQ ID NOS: 14110
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 FGGSLRRQDENFDGKIKAI 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Staphylococcus aureus
US-09-815-242-5704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.89
Matches 7; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model t OM protein September 15, 2003, 17:18:16 Run on:

6; Search time 11.7 Seconds (without alignments) 213.708 Million cell updates/sec

US-09-544-664-1 Perfect score:

26 138 1 NLWAAQRYGRELRRMSDEFEGSFKGL Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 of hits satisfying chosen parameters: Total number

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	bad protein - mous	inter-alpha-trypsi	hypothetical prote	inter-alpha-inhibi	2-dehydro-3-deoxy-	floral homeotic pr	spermidine/putresc	probable threonine	77	Ig kappa chain - h	annexin P35 - maiz	transforming prote	oxidoreductase, so		oxaloacetate decar	oxoglutarate dehyd			Antho-RFamide prec	cal p	_;> <sub>1</sub>	inter-alpha-trypsi	hypothetical prote	DNA-directed RNA p	conserved hypothet	neuropeptide Pol-R	Antho-RFamide neur	hypothetical prote	NADH dehydrogenase
SOMMANIES	qi	A55671	JC5575	D70760	\$54354	538185	A42095	C84338	A96753	E83517	S40376	T02975	C36365	F72289	T08545	G82308	F82668	B96695	T02961	A44308	T09486	T35440	IYHU2	T24806	A81393	669510	S43852	17	~	G83314
	DB														~															
	Length	204	946	223	946	370	232	374	516	453	134	314	206	220	526	597	967	5138	314	435	1140	399	946	1164	1378	261	287	334	562	905
op (	Match	100.0	39.1	38.4	38.4	37.7	37.0	36.2	36.2	35.5	35.1	35.1	34.8	34.8	34.8	34.1	34.1	34.1	33.7	33.7	33.7	33.3	33,3	33,3	33.3	33.0	33.0	33.0	33.0	33.0
	Score	138	54	53	53	52	51	20	20	49	48.5	48.5	48	48	48	47	47	47	vo.	46.5	Q	46	46	46	46	വ	45.5	L.	45.5	45.5
4	Kesuit No.	Н	7	m	ব	2	9	7	∞	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

chlorocruorin chai	conserved hypothet	conserved hypothet	xo dund uoi moipos	oxaloacetate decar	oxaloacetate decar	oxaloacetate decar	probable membrane	env polyprotein -	hypothetical prote	NADH dehydrogenase					
559899	F83201	H95406	B44465	AB0509	AE0909	A28088	S52675	VCLJG4	T19472	128811	T15566	T01993	D83264	AG1482	G91024
7	7	N	7	7	~	7	7	~-1	7	~	C)	~	a	~	7
165	295	346	591	591	591	969	715	864	1263	1557	2325	75	455	536	910
32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.2	32.2	32.2	32.2
45	45	£ €	45	45	45	45	45	45	45	45	45	44.5	44.5	44.5	44.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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bad protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Actes: Mus musculus (house mouse)
C;Actesion: A55671
R;Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and E A;Reference number: A55671; MuID:95136361; PMID:7834748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779 C;Keywords: heterodimer
                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-204 <YAN>
RESULT 1
                                        A55671
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promot

Gaps ò 2; Length 204; Indels ö 100.0%; Score 138; DB 2; ilarity 100.0%; Pred. No. 7e-13; Conservative 0; Mismatches ( Local Similarity les 26; Conserv Query Match Best Local Si Matches 26;

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g δŽ

RESULT JC5575

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster (5) Species: Mesoricetus auratus (golden hamster)
C; Stocken: 125, 71-82, 1997
R; Nakatani, T.; Sizuki, Y.; Yamamoto, T.; Sinohara, H.
A; Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs in inhibitor heavy chain family.
B; Reference number: UC5574; MUID:97420688; PMID:9276673
A; Molecule type: mRNA
A;

A/Accession: PG4485
A/Molecule type: protein
A/Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C/Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important role for panceatic cancer.
C/Superfamily: inter-alpha-trypsin inhibitor complex component II
F/261-264,717-916/Disulfide bonds: #status predicted

Score 54; DB 2; Length 946; Pred. No. 8.8; 39.18; 34.68; Query Match Best Local Similarity a

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"Increa" homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
N.Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
(Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: A42095; S52633; T47593
R; Jack, T; Brockman, L.L.; Meyerowitz, E.M.
A; Jitle: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is A; Reference number: A42095; MUID:92154682; PMID:1346756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: aldehyde-lyase; carbon-carbon lyase
A; Description: alcohyde-lyase; carbon-carbon lyase
A; Vote: first step in shikimate pathway
C; Superfamily: phospio-2-dehydro-3-deoxyheptonate aldolase
C; Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S46130
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Crossides: 1-370 < AIGS
A; Crossine type: A; MID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR; R; Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
Gene 113, 67-74, 1992
A;Title: The complete sequence of a 6794 bp segment located on the right arm of chron A;Reference number: S38185; MUID:94078675; PMID:8256522 A;Accession: S38185
                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-370 <ALJ>
A,Cross-references: EMBL-236118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBR;
R;A491e, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouset, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyra. Reference number: JN0322; M0ID:92225349; PMID:1346717
A:Accession: JN0322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Mosidoss: 1.204,208-370 < KUE>
A; Residoss: 1.204,208-370 < KUE>
A; Cross-references: EMBL:X61107
B; Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
B; Ruenzler, M.; Sa48-5589, 1993
A; Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifur A; Reference number: A48651; MUID:99374850; PMID:8366040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                             A:Cross_references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102 R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M. submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:ARO4
A;Cross-references: SGD:S0000453; MIPS:YBR249c
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                                                                                                             A; Status: translation not shown
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 352-370 <KU2>
A; Cross-references: GB:X61107
                                                                                                                                                                                                                                                                                       A;Reference number: $45906
A;Accession: $46126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S45940
                                                                                                                                                                   A; Residues: 1-370 <DOI>
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                                                                                                                                          A; Molecule type: DNA
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C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C;Accession: 54555, Jegs
B;Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem, J. 306, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: A;Reference number: S54353; M(ID:95194326; PMID:7534067
A;Recession: S54354
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                             C;Accession: D70760
R;Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.: Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandteam, M.A.; Rogers, J.; Rutter, S.; Seeger, R.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; FMID:9634230
A;Accession: D70760
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911; A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces o N.Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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C;Date: 31-Dec-1993 #text_change 03-Jun-2002
C;Accession: S38185; S46126; S46130; JN0322; B48651
E;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.

geast 9, 1131-1137, 1993
                                                                                                                                                                                                                                                                                       hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:9695634
II
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                Gaps
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A)Cross-references: EMBL:X70392; NID:g695633; PIDN:CAA49842.1;
C)Superfamily: inter-alpha-trypsin inhibitor complex component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 946;
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                   Indels
                12;
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2.8;
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                Mismatches
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Pred. No.
                                                                                                             212 NVWIIEPQGMRFLHVPDTFEGHFQGV 237
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Pred. No.
                                                                         26
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                                                                             1 NLWAAQRYGRELRRMSDEFEGSFKGL
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                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 NLWAADRYNRAIARGHD 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.4%;
58.8%;
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34.6%;
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Best Local Similarity 58.8
Matches 10; Conservative
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            Conservative
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-223 <CC
            9
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                Matches
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96753
T;Theologis, A:; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Ching, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.P.; Highes, B.; Huizar, L.
Nature 408, 816-820, 2000
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vebrer, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A96753
A;Status: preliminary
A;Accession: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PAO C; Species: Pseudomonas aeruginosa aeruginosa (c; Species: Pseudomonas aeruginosa (strain PAO C; Species: Pseudomonas aeruginosa (strain PAO C; Species: Pseudomonas aeruginosa (strain PAO C; Species: Pseudomonas aeruginosa (strain PAC) R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Stover, S.; Viann, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Ras, A.; Larbig, K.; L. in Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: E83517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AAG04420.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1031
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C;Genetics:
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 540376
Eur. J. Immunol. 23, 3248-3271, 1993
A;Titler: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 NLFWAERFGKQYLQMNDLWVKHCGISHTGSFKDL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.5%;
55.6%;
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WASERQGREEELRRLASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.5
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Conservative
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Best Local Similarity
Matches 12; Conserv
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A, Molecule type: DNA
A, Residues: 1-453 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-516 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain - human
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A;Map position: 1
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S40376
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   A;Residues: 1-232 cJAC>
A;Cross-references: GB-1886357; NID:g166607; PIDN:AAA32740.1; PID:g166608
A;Experimental source: petals, stament standard from NCBI backbone (NCBIN:82520, NCBIP:82521)
B;Okamoto, H.; Yano, A.; Shiralshi, H.; Okada, K.; Shimura, Y.
B;Okamoto, H.; Yano, A.; Shiralshi, H.; Okada, K.; Shimura, Y.
B;Okamoto, H.; Yano, A.; Shiralshi, H.; Okada, K.; Shimura, Y.
A;Diath Mol. B;Ol. 26, 465-472, 1994
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid A; Accession: S52633; MUID:95036018; PMID:7948893
A;Accession: S52633; MUID:95036018; PMID:7948893
A;Accession: S72633; MUID:95036018; PMID:7948893
A;Accession: A;As and A
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C; Date: 0.02 Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: C8438
R; Ng. W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Laithauser, B.; Realler, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable, Jung, K.H.; Alam, M.; Freitas, Y.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable, Droc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Atthore: Hou, S.; Daniels, G.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.W.; Li. A; Reference number: A84160; MulD:20504483; PMID:11016950
A; Accession: C8438
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-374 <STO>
A; Coss-references: GB:AE004437; NID:910581314; PIDN:AAG20071.1; GSPDB:GN00138
C; Gene: potA2
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Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 QRYG-----RELREMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2%;
76.9%;
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Best Local Similarity 76.9
Matches 10; Conservative
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Ricurien, G.; Dumas, R.; Ravanel, S.; Douce, R. FEBS Lett. 390, 85-90, 1996 A; Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi A; Reference number: S71362; MUID:96314555; PMID:8706836 A; Accession: S71362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE001772; GB:AE000512; NID:94981693; PIDN:AAD36230.1; PID:9498
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                               R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                              Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               threonine synthase (EC 4.2.3.1) precursor - Arabidopsis thaliana N.Alternate names: protein F27B13.80 (S)Species: Arabidopsis thaliana (mouse-ear cress) (C)Apecies: Arabidopsis thaliana (mouse-ear cress) (C)Accession: 10.101-1999 #sequence_revision 11.5un-1999 #text_change 03-5un-2002 (C)Accession: 708545; S71362; S74307 (R)Bevran, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, Submitted to the Protein Sequence Database, May 1999 (A):Reference number: 216442
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A;Accession: S74307
                                                                                                                                                                        C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: F72289
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F:1-39/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:40-526/Product: threonine synthase #status experimental <MAT>
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                                                                                                                                               sol/devB family - Thermotoga maritima (strain MSB8)
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A; Residues: 1-1526 < GEV)
A; Cross-references: EMBL:ALO50352; GSPDB:GNO0062; APSP:F27B13.80
A; Experimental source: cultivar Columbia; BAC clone F27B13
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Pred. No. 15;
8; Mismatches 7; Indels
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Pred. No. 37;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AAQRYGRELRRMSDEFEGSFKGL 26
169 REIRRMNKEQEGRSKG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: TM1154
C;Superfamily: yeast SOL3 protein
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35.3%;
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Matches 8; Conservative
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A; Residues: 'L', 3-526 <CUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-220 <ARN>
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transforming protein homolog MRAS3 - Rhizomucor racemosus
C;Species: Rhizomucor racemosus
R;Casale; Will: McConnell D.G; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A;Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhib
A;Reference number: A36365; MUID:91061774; PMID:1701021
A;Rocasion: C36365
A;Status: preliminary
A;Residues: 1-206 CCAS
A;Cossreferences: GB:MS5177
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleotide binding; P-10op
F;11-126/Domain: translation elongation factor Tu homology
C;Keywords: GTP binding MKXD motif A; (P-10op)
F;123-126/Region: nucleotide-binding MKXD motif
F;13-126/Region: GTP-binding NKXD motif
F;13-126/Region: GTP-binding NKXD motif
F;13-126/Region: GTP-binding NKXD motif
F;13-126/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annexin P35 - maize

C;Species: Zea may9 (maize)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000

C;Accession: T02975

R;Battey, N.H.; James, N.C.; Greenland, A.J.

Plant Physiol: 112, 1391-1396, 1996

A;Title: CDNA isolation and gene expression of maize annexins P33 and P35.

A;Accession: T02975

A;Accession: T02975

A;Accession: T02976

A;Coss-references: EMBL:X96245; NID:g1370602; PIDN:CAA66901.1; PID:g1370603

A;Experimental source: cultivar clipper; root tip
C;Superfamily: annexin I; annexin repeat homology
F;14-85/Domain: annexin repeat homology <AXR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                  ..
H
                     A;Residues: 1-134 <KLE>
A;Cross=references: PMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer: immunoglobulin
F;34-113/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                          Length 134;
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                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                          BB
                                                                                                                                                                                                    Score 48.5; DB Fred, No. 7.8; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                58 WFRORPGRSPRRLIYNVSKRDSGVSDRFSGSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 19;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.5;
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54 AEAYGKELLRALGDEIHGKFE 74
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47.6%;
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38.2%;
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Best Local Similarity 47.65
Matches 10; Conservative
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Best Local Similarity
Matches 13; Conserv
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Matches 10; Conserv
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RESULT 15

GRADOM Category 15

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Search completed: September 15, 2003, 17:27:00 Job time: 12.7 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ||:|: :||| ||:
272 YFREVRKKYAKFEGQLKGV 290
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model,

September 15, 2003, 17:16:551; Search time 6.12857 Seconds (without alignments) 199.507 Million cell updates/sec Run on:

US-09-544-664-1 138 1 NLWAAQRYGRELRRMSDEFEGSFKGL 26 Title: Perfect score: Sequence:

BLOSUM62 . Gapext 0.5 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	_				Q61703 mus musculu		P35632 arabidopsis		O62992 ledum palus					m													Pl3187 klebsiella		P05886 simian immu		-	3900	O54918 mus musculu
SUMMARIES	ID			BAD_HUMAN							MATK_RHOFR		RMU		6PG																	_	_	BIM_MOUSE
	Length DB																												653 1				907 1	196 1
о¥О	Query Match I	100.0	100.0	82.6	39.1	38.4	37.7	37.0	36.2	35.9	35.9	35.9	35.5	34.8	34.8	34.8	34.8	34.1	33.7	33.7	33.3	33.3	33.0	33.0	33.0	32.6	32.6	32.6	32.6	32.6	32.6	32.2	32.2	31.9
	Score	138	138	114	54	53	52	51	50	49.5	49.5	49.5	49	48	48	48	48	47	46.5	46.5	46	46	45.5	45.5	45.5	45	45	45	45	45	45	44.5	44.5	44
	Result No.	7	5	m	4	Ŋ	9	7	æ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

088498 rattus norv 08x2c6 escherichia P50465 escherichia 08x862 salmonella 08x206 salmonella 27757 simian immu P2775 sim
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# ALIGNMENTS

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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S->A: NO PHOSPHORYLATION,
S->A: NO PHOSPHORYLATION,
S->A: NO PHOSPHORYLATION, INTERACTS WITH
BCL-X(L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein Kinase A (CARK) phosphorylation.
SIMILARITY: Contains 1 Bcl.-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PHOSPHORYLATION (BY PKA AND PKB).
PHOSPHORYLATION (BY PKA AND PKB).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoctation update)
BCl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 138; DB 1; Length 204; 100.0%; Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=21109372; PubMed=11161472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE-98194755; PubMed-9535132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. Lett. 243:137-140(1998)
                                                                                                                                                                                                                                                                             PIR; A55671; A55671.

HSSP; Q92934; 1G57.

MGD; MGI:1096330; Bad.

InterPro; IPR000712; Bc12_BH.

PROSITE; PS01259; BH3; FALSE_NEG.

Apoptosis; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA; 22080 MW;
                                                                                                                                                                                                                                                            EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                   161
112
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les 26; Conserv
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MUTAGEN
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Matches
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ID BAD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

"Functional characterization of two splice variants of rat BAD and
their interaction with Bcl-w in sympathetic neurons.";

Mol. Cell. Neurosci. 7:99-106(2001).

-! FUNCTION: Promotes cell death. Successfully competes for the
binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level
of heterodimerization of these proteins with BAX. Can reverse the
death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
similarity). Appears to act as a link between growth factor
receptor signaling and the apoptotic pathways.

-! SUNGNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
x(L), Bcl-2 and Bcl-w. Also binds protein SlOADIO. The Ser-
-! SUBCELLUARS LOCATION: Outer mitochondrial membrane. Upon
phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name Decreases and tissues tested, including brain, liver, spheen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

-!- DOMAIN: Intact Ball domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apototic members of the Bcl-2 family.

-!- PIM: Phosphorylated on Ser-113 in response to survival stimuli.

Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-166, a site within the BH3 domain. leading to the release of Bcl-x(L) and the promotion of cell survival.

Ser-137 is the major site of AKTVPKB phosphorylation, Ser-156 the major site of Protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPRPKSAGTATOMRÓSASWTRIIOSWWDRNLGKGGSTPSQ
-> EELTYSVEFLPVRALAMEGWPLLWSFQSPPHILPPTPP
EVAMFPLRYWTALRRLC (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEINS. NO EFFECT ON HETERODIMERIZATION WITH BCL2 NOR WITH PROTEIN P11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH 14-3-3 PROTEINS.
S->A: NO HETERODIMERIZATION WITH 14-3-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S->A: NO EFFECT ON HETERODIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY PKA AND PKB)
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PHOSPHORYLATION (BY PKA AND PKB)
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PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
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7AFA71DAE9CF4A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Alpha;
IsoId=035147-1; Sequence=Displayed;
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22228 MW;
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113
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205 AA;
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Proc. Natl. Acad. Sci. U.S. A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                         15-SEP-2003 (Rel. 40, Last Sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BCl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yin D.X., Li 2., Huang B., Chen S., Zhou H.; A human protein that interacts with Bcl-2 and have homology to mouse
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bone marrow;
MEDLINE=98049554; PubMed=9388232;
MEDLINE=98049554; PubMed=9388232;
Chilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,
Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
"Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
                                           ò
  Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97083574; PubMed-8929532; Wang H.-G., Rapp U.R., Reed J.C.; "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
100.0%; Score 138; DB 1;
100.0%; Pred. No. 1.6e-13;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2] SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
                                                                                                                                                                                                                         168 AA
                                                                                                       141 NIWAAQRYGRELRRWSDEFEGSFKGL 166
                                                                                1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                                                                                         PRT;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                      092934; 014803;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequ
                                           26; Conservative
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                         BAD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  imilarity).

- GUSCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.

- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

- DOMAIN: Intract BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

- PTM: Phosphorylated on Ser-75 in response to survival stimuli. Subsequent phosphorylation on Ser-99 promotes heterodimerization with A-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.

Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-:- SIMILARITY: Contains 1 Bc1-2 homology 3 (BH3) domain.
-:- SIMILARITY: BELONGS TO THE Bc1-2 FAMILY.
-:- CAUTION: Ref. 1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                        mutagenesis, and biophysical studies."

Protein Sci. 9:228-2534(2000).

Protein Sci. 9:238-2534(2000).

Protein Sci. 9:238-2534(2000).

Protein Sci. 9:238-254(2000).

Protein Sc
STRUCTURE BY NMR OF 103-127.
MEDITNE-21073561; PubMed=1126674;
PETICS A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Marayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                  complex formation from structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mis. OCSIDE, C. Cytoplasm; NAS. GO; GO:0005737; C:cytoplasm; NAS. GO; GO:0005741; C:mitochondrial outer membrane; NAS. GO; GO:0005515; F:protein binding activity; NAS. GO; GO:0006917; P:naporpotic program; TAS. GO; GO:0006917; P:induction of apoptosis; NAS. InterPro; IPR000712; BG12_BH. PROSITE; PS01259; BH3; FALSE_NEG. Poptosis; Phosphorylation; Polymorphism; 3D-structure. DOMAIN 110 124 BH3.
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A -> S (in dbSNP:3729933).
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18392 MW; 69FD8D27DDEE3241 CRC64;
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EMBL; AF021792; AAB72092.1; --
EMBL; AF031233; AAB88124.1; --
EMBL; EC001901; AAH01901.1; --
PDB; 1G55; 07-FEB-01.
                                                                                                                      Fesik S.W.;
"Rationale for Bcl-xL/Bad peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
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168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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SMART; SM00327; VWA; 1.
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       NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"Moleoular cloning and sequencing of conka encoding three heavy-chain
precursors of the inter-alpha trypsin inhibitor in Syrian hamster:
implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HI, HA OR H3) AND ONE LIGHT (PALM).

BIKUNIN. INTER-ALPHA-IMILIBITOR (I-ALPHA-I) IS COMPOSED OF HI, H2
BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-I) OF H2 AND
BIKUNIN, AND PRE-ALPHA-LIKE INHIBITOR (P-ALPHA-I) OF H3 AND
FRE-ALPHA-INGROWN (R-ALPHA-II) OF H3 AND
FRE-ALPHA-II OF H3 AND BIKUNIN VIA A CHONDROITIN
FRE-ALPHA-II OF THEIR C-TERMINAL ASPARTATE (BI
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING PROTEIN BETWEEN HYALUKONAN AND OTHER MATRIX PROTEIN, MICHDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hamster urine and plasma.";
J. Biochem. 120:145-152(1996).
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto T , Yamamoto K , Sinohara H .; "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                         6
                                         Indels
                                      ..
       Pred. No. 5e-10;
                                                                                                                                                                                                                                                                                                                                                              946 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ITH FAMILY.
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97018241; PubMed=8864857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97420688; PubMed~9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ivy chain family.";
Biochem. 122:71-82(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D89286; BAA13939.1; -
PIR; JC5575; JC5575.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
91.78;
                                         22; Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus
                                                                                                                                                                                                                                                                                                                                                              TTH2_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy
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                                         Matches
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                                                                                                                                            BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy chain H2) (Inter-alpha-inhibitor heavy chain 2).
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                   Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 1; Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
V -> Y (IN REF. 2).
E -> I (IN REF. 2).
V; CA8BF565458E7B2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .)
CHONDROITIN 4-SULFATE,
                                                                                                                                                                                                                                                                                 VWFA.

N-LINKED (GLCNAC. .

N-LINKED (GLCNAC. .

N-LINKED (GLCNAC. .

N-LINKED (GLCNAC. .
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-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.4;
5; Mismatches
                                                                                                                                                                                                                                                  SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 NVWIVELQGMRFLHVPDTFEGHFQGV 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.1%;
34.6%;
VWFA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 34.6 ses 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510
                                                                                                         18
54
702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946 AA;
   PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                              Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CHAIN
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                                                                                                             SIGNAL
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Yeast 9:1131-1137(1993).
                                                                                      STRAIN-S288c;
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                                                     SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

WINDLINE-92225349; PubMed=1348717;

Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;

Kloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";

Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doignon F., Biteau N., Aigle M., Crouzet M., "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUTPase in a yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomyotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.4%; Score 53; DB 1; Length 946; 34.6%; Pred. No. 4.8; ive ∴5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuenzler M.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
; 40DB6716433ED9DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WFA
                                                                                                                                                                                        MGD; MGI:86619; Itih2.
InterPro; 1PR006587; VIT.
InterPro; 1PR006387; VWF_A.
Pfam; PF00002; VWA; 1.
SMART; SM00609; VIT; 1.
SMART; SM00377; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARO4 OR YBR249C OR YBR1701.
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                                                                                                                                     EMBL; X70392; CAA49842.1;
PIR; S54354; S54354.
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Best Local Similarity 34.6
Matches 9; Conservative
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54
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REVISIONS TO 205-207.
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308
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P32449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGD; S0000453; ARO4.
GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA.
InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHPI/KDSA.
                                                                    FUNCTION: STERROSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ERYTHROSEA-4-PHOSPHATE (E4P) GIVING RISE TO 3-DECXI-D-
ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAP).
CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
phosphate + H(2)0.
BNZYME REGULATION: INHIBITED BY TYROSINE.
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P353.ARTH
STANDARD; QS703; Q98014; Q98015; Q98016; Q98017;
Q98018; Q98019; Q98020; Q98021; Q98014; Q98015; Q98016; Q98017;
Q98018; Q98019; Q98020; Q98021; Q98021; Q98013;
Q1-JUN-1994 (Rel. 29, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
Floral homeotic protein APPTALA3.
AR3 OR AT3654340 OR T12E18_30.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Virigilantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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Jack T., Brockman L.L., Meyerowitz E.M.;
"The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
box and is expressed in petals and stamens.";
Cell 68:683-697(1992).
                                                                                                                                                                                                                                                                                                                                                PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
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                                                                                                                                                                                                                                                                                                                                                                                         first step.
-i-INDUCTION: By amino acid starvation.
-i-STMILMSTITY: BELONGS TO CLASS-I DAHP SYNTHEFASE FAMILY.
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TIGRFAMS; TIGR00034; arofeH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%; Score 52; DB 1; Length 370; 47.6%; Pred. No. 2.4; 5; Mismatches 6; Indels
Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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Matches 10; Conservat
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NCBI_TaxID=3702;
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from Arabidopsis thaliana sequences of known biological
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AF115809;
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                                                                                                                                                                                                    PubMed=8643482;
                                                                                   PubMed=8565821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    floral organs.
                    unction.
                                                                  FUNCTION
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   RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutury M., Grivell L., Mache R., Pujdomenech P.,
RA Delseny M., Boutury M., Aristiquenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincher M., Maneller-Auer S., Gabbe C., Fuchs M., Benes V.,
RA Windelmann R., Kranz H., Woss H., Holland R., Brandt P., Nyakatura G.,
RA Conrad A., Hornischer K., Rauer G., Loehnert T.-H., Nordsiek G.,
RA Conrad A., Hornischer K., Rauer G., Loehnert T.-H., Nordsiek G.,
RA Wavarro P., Collado C., Perez-Perez A., Otterna, C., Climent J.,
RA Ge Haan M., Maarse A.C., Alcarsz A., Otterta B., Masuy D.,
RA Mondort A., Argiriou A., Flores M., Liquori R., Vitale D., Mewes H.-W.,
RA Mondort A., Argiriou A., Flores M., Liquori R., Vitale D.,
RA Mondort A., Argiriou A., Flores M., Liquori R., Vitale D.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fulin C., Shea T.P.,
RA Rosey T., Rizzo M., Walts A., Utterback T., Fulin C., Van Aken S.,
RA Peress D., Lin X., Nierman W.C., Salberg S., White O., Venter J., Asamicu E.,
RA Sasamoto S., Kinnz T., Idesawa K., Ravashima K., Kishida Y.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yasuda M., Yasuda M., Tabata S.,
RY Watanabe A., Yasuda M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S.,
RY Natura A.R., Rama M., Yasuda M., Tabata S., Rama M., Tabata S.,
RY Natura A.R., Rama M., Rama M., Tabata S.,
RY Natura A.R., Rama M., Rama M.
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MEDLINE-99311297; PubMed=10382288;
MEDLINE-95311297; PubMed=10382288;
Brunel D., Froger N., Pelletier G.;
"Development of amplified consensus genetic markers (ACGM) in Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cowa (RAFLs) sequenced by the
                                                                                                                                                                                                                                                             Purugganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci: departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
                                 STRAIN-cv. Landsberg erecta;
MEDIJINE-55036018; PubMed-7948893;
Okamoto H., Tano A., Shiraishi H., Okada K., Shimura Y.;
Gemetic complementation of a floral homeotic mutation, apetala3,
with an Arabidopsis thallana gene homologous to DEFICIENS of
                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS.
STRAIN-cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2, cv. Chi-1, cv. Co-1, cv. Collumbia, cv. Corsacalla-1, cv. Cvi-0, cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta, cv. Li-3, cv. Li-8, and cv. Lisse;
MEDLINE-99126449; PubMed-9927474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Troukhan M., Alexandrov N., Lu Y.-P., Flavell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016720; PubMed=11130713;
                                                                                                                                  Plant Mol. Biol. 26:465-472(1994).
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 [2]
SEQUENCE FROM N.A.
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                                                                                                                    Antirrhinum majus.
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Feldmann K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:252-29(2001).

1- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILIARA that is required for autoregulation of both Ap3 and PI genes. AP3/PI heterodimer interacts with APETALA or SEPALMARA to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
                                                                                                                                  Krizek B.A., Meyerowitz B.M.;
"The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function.";
Development 122:11-22(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                Riechmann J.L., Krizek B.A., Meyerowitz E.M.;
"Dimerization specificity of Arabidosis MaDS domain homeotic proteins APPTALA1, APPTALA3, PISTILATA, and AGAMONS.";
Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1. SUBCELLUIAR LOCATION: Nuclear.
-1. TISSUE SPECIFICITY: Expressed in petals and stamens.
-1. INDUCTION: Positively regulated by the meristem identity proteins APETALA and LEARY with the cooperation of UFO.
-1. MISCELANBROG'S Mutations in APS cause transformation of petals into sepals and stamina into carpels.
-1. SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11206550; Honma T., Goto K.; Romma T., Goto K.; "Complexes of MaDS-box proteins are sufficient to convert leaves into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11283333;
Ng M.; Yanoffsky M.F.;
"Activation of the Arabidopsis B class homeotic genes by APETALAL.";
Plant Cell 13:739-753(2001).
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AAD51892.1;
AAD51893.1;
AAD51894.1;
AAD51895.1;
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EMBL; D21125; BAA04665.1; -.
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AAD51896.1;
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AAD51898.1;
Genome 42:387-402(1999).
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                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF115802; AF115803; A
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DORRANDOR AND DESCRIPTION OF A STATE OF A ST

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EMBL; AB012751; BAA25872.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATK_LEDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AD 000292
DT 15-SEP
DT 15-SEP
DT 15-SEP
DT 15-SEP
DE MATURA
GN MATK.
GN M
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KRINE-22388257; PubMed-12477932;

Krinesberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeoleng B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Robins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M. J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Warny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Flowering; Transcription regulation; Activator; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-BOX.

COLLED COLL (POTENTIAL).

K -> R (in strain cv. Lisse).

M -> T (in strain cv. Bretagny).

N -> D (in strain cv. Corsacalla-1).

T -> S (in strain cv. Li-8).

L -> V (in strain cv. Kas-1).

E -> K (in strains cv. Chi-1 and cv. Gr-3).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; DNA-binding; Coiled coil; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Protein CSorf5 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                851 AA.
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EMBL; AFILS610; AAD51899.1; --
EMBL; AFILS611; AAD51900.1; --
EMBL; AFILS613; AAD51900.1; --
EMBL; AFILS613; AAD51902.1; --
EMBL; AFILS614; AAD51903.1; --
EMBL; AV070397; CAB81799.1; --
EMBL; AV070397; AAA6419.1; --
EMBL; AV742590; AAA4893.1; --
EMBL; AV742590; AAA13159.1; --
EMBL; AF40556, AAA13159.1; --
EMBL; AF40565, AAA13159.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam: PF01486; K-box; 1.
Pfam: PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.0%:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P11746; 1MNM.
TRANSFAC; T01776; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEO5_MOUSE
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VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M.,
Butterfield Y.S.M., Krzywinski M.I., Skalska J., Smailus D.E.,
Schnerch A., Schelm J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
buman and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SIMILARITY: Belongs to the FAM13 family.
-!- SIMILARITY: Contains I Rho-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-i- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          watch 36.2%; Score 50; DB 1; Length 851; Local Similarity 45.5%; Pred. No. 12; local Similarity 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Investigation of sectional relationships in the genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851 AA; 97054 MW; C2B26669FB6DB2CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhododendron (Ericaceae) based on matK sequences.
Shokubutsu Kenkyu Zasshi 73:143-154(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |: ::||:| || || :|
LWKARAEKKKLRKMLREFEEAF 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LWAAQRYGRELRRMSDEFEGSF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ledum palustre (Wild rosemary).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC031465; AAH31465.1; -.
InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
PROSITE; PS50238; RHOGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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GTPase activation.
DOMAIN 23 212
189 256
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8

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RESULT 12
RMUC_PSEAE
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                                                                                                                                                                                                         Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
NCBI_TaxID=49622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matk sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
--- FUNCTION: Probably assists in splicing chloroplast group II introns (By shmilatity).
--- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.9%; Score 49.5; DB 1; Length 506; 36.7%; Pred. No. 8.2;
                                                                                                                                                            DB 1; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60534 MW; ADA44B25E92436E8 CRC64;
                                                                                                               CFEA926307DAC85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 AA
                                                                                                                                                                                                                                                                           :||| :| : || | 393 VWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                                                           506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 VWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                          35.9%; Score 49.5; DI 36.7%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LWAA-----QRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                 2 LWAA-----QRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhododendron ferrugineum (Alpenrose).
InterPro; IPR000442; Intron_maturse2. InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01344; MatK_N.
MatK_N.
MRNA processing; Chloroplast.
SEQUENCE 506 AA; 60412 MW; CFEA92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _MATK_RHOTS STANDARD;
062991;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB012741; BAA25862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Local Similarity 36...,
Best Local Similarity
The Conservative
                                                                                                                                  Query Match
Best Local Similarity 36./*,
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           MATK_RHOFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATK_RHOTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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STRAIN-ARCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
STRAIN-ARCC 15692 / PAO1;
STRAIN-ARCC 15692 / PAO1;
STRAIN-ARCC 15692 / PAO1;
STRAIN-ARCC 15692 / PAO1;
STRAIN X: O'LT, Ervin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Golltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                           Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, Ericales, Ericaceae, Ericoideae, Rhodoreae, Rhododendron.
                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-:- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-:- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Protecobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.9%; Score 49.5; DB 1; Length 506; 36.7%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60569 MW; AEE12FF8809C223E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
DNA recombination protein rmuC homolog.
RMUC OR PA1031.
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LWAA-----QRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB012750; BAA25871.1; -.
Interpro; IPR000442; Intron_maturse2.
Interpro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                        Rhododendron tsusiophyllum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=49629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.
                                                                                                                                                                          Chloroplast.
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us-09-544-664-1.rsp

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InterPro; IPR006148; Gluc_gal_isom.
InterPro; PR005900; Phosphoqluconlac.
Pfam; PF01182; Glucosamine_iso; 1.
TIGRRAMS; TIGR01198; pg1; 1.
                                                                              Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
PRINTS; PR00449; RAC: ....SMART; SM00173; RAS; 1...mrcR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001772; AAD36230.1; -. PIR; F72289; F72289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Complete proteome.
SEQUENCE 220 AA; 25325 MW;
                                                                                                                                                                                                               23408 MW;
                                                                                                                                                                                                                                                                                                                                                                            34.8%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                  10 RELRRASDEFEGSFKG 25
                                                                              GTP-binding; Prenylation;
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                               23
67
125
46
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHOGLUCONATE.
                                                                                                                  63
122
122
13
38
202
205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; TM1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6PGL_THEMA
09X0N8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                 SEQUENCE
                                                                                             NP_BIND
NP_BIND
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
6PGL_THEMA
                                                                                                                                                                                              LIPID
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         SORRETTERS
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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its oncent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       FUNCTION: Involved in DNA recombination (By similarity).
SIMILARITY: BELONGS TO THE RMUC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91061774: Pubmed=1701021;
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
Wilch exhibits striking similarity to human ras genes.";
Mol. Cell. Biol. 10:6654-6663(1990).
-!- BNZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GIRNINE
NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GIPASE-
ACTIVATING PROTEIN (GAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE SMALL GIPASE SUPERFAMILY. RAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Plasma membrane.
-!- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
GERMLING AND YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
Eukaryota; Fungl; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%; Score 49; DB 1; Length 453; 55.6%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                           PIR: B8517; E8317.
InterPro: IPR003798; D0F195.
Pfam: PF02646; Rmuc; 1.
DOMAIN recombination; Coiled coil; Complete proteome.
DOMAIN 16 201 COILED COIL (POTENTIAL).
SEQUENCE 453 AA; 51539 MW; IE7EA97E82EC5E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro: IPR003577; GTPase_Ras.
Interpro: IPR001806; Ras_trnsfirmug.
Interpro: IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 WASERQGREEELRRLASE 82
                                                                                                                                                                                                                                                          EMBL; AE004535; AAG04420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 WAAQRYGR--ELRRMSDE 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 55.6 ses 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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HSSP; P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ras-like protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAS3_RHIRA
P22280;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mucor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-WESB (J. DSW 3109),
MEDLINE-99287316; PubMed-10360571;
A Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Melson W.C., Kerchum K.B.,
A Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Stewart A.M., Sutton G.G., Pleischmann R.D., Bisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
I genome sequence of Thermotoga maritima.";
I seture 399:223-229(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phospho-D-gluconate.
-!- PATHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACIOSAMINE-6-PHOSPHATE ISOMERASE FAMILY: 6-PHOSPHOGLUCONOLACIONASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga. NCBL_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                               .;
0
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                                                                                                                                                                                                                                                                                DB 1; Length 205;
                                                                                                                   EFFECTOR REGION (PROBABLE).
FARNESYL (BY SIMILARITY).
DBF086466F090F50 CRC64;
                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9BOFD07EE01E60C3 CRC64;
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
6-Phosaboqueonolactonase (BC 3.1.1.31) (6PGL).
PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                Score 48; DB 1.
Pred. No. 5.1;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AA.
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PROSITE; PS00165; DBHYDRATASE_SER_THR; 1.
Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme; Chloroplast; Transit peptide.
TRANSIT 1 40 CHLOROPIAGT NO CHLOROPIAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metabolically regulated by photosynthesis-related signals or by nitrogenous compounds."; nitrogenous compounds."; plant Sci. 157:43-50(2000).
-- CATALNTIC ACTIVITY: O-phospho-L-homoserine + H(2)0 = L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate.
-:- COFACTOR: Pyridoxal phosphate (By similarity).
-:- COFACTOR: Pyridoxal phosphate (By similarity).
-:- ENZYME REGULATION: Allosterically activated by S-adenosyl-methionine (SAM) (By similarity).
-:- PATHWAR: Threconine biosynthesis; last step.
-:- SUBGULGIAR LOCATION: Chloroplast (By similarity).
-:- SUBCELLGIAR LOCATION: Chloroplast (By similarity).
-:- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                 Solanum tubercoum (Orotato).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Casazza A.P., Basner A., Hoefgen R., Hesse H.; "Expression of threonine synthase from Solanum tuberosum L. is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHLOROPLAST (BY SIMILARITY).
THREONINE SYNTHASE.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.8%; Score 48; DB 1; Length 519; 35.3%; Pred. No. 14; tive 6; Mismatches 8; Indels
 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114C0979CD231464 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSD-----EFEGSFKGL 26
                                                                                                                                                                   519 AA.
 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 15, 2003, 17:22:59 Job time: 7.12857 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF082894; AAF74984.1; -.
HSSP; Q9S7B5; IB5X.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydxtse.
InterPro; IPR00456; Thr_synthase.
Pfam; PF00291; PALP; 1.
                                                            4 AAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                     PRT;
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519 AA; 57412 MW;
                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 35.3
Matches 12; Conservative
 8; Conservative
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Leaf;
PubMed=10940468;
                                                                                                                                                                   THRC_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                       Q9MT28;
                                                                                                                                RESULT 15
THRC_SOLTU
 Matches
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Perfect score:

on:

Sequence:

Scoring table:

Searched:

Database

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294633 anopheles g
097407 anopheles g
047148 menziesla c
047149 rhododendro
047171 rhododendro
06396 rhododendro
062972 rhododendro
062978 rhododendro
062978 rhododendro
062978 rhododendro
047155 rhododendro
047157 rhododendro
047157 rhododendro
047157 rhododendro
047157 rhododendro
047157 rhododendro
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047170 rhododendro
047174 rhododendro
062983 rhododendro
062980 rhododendro
062981 rhododendro
                                                                                    O9hnz9 halobacteri
O9ssp5 arabidopsis
O8k2h3 mus musculu
                                                                      chimpanzee
halobacteri
                                               Q8k316 mus musculu
                         shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii, Neopteryqii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
MEDILINE-20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 87; DB 13; Length 14 ilarity 65.2%; Pred. No. 5.3e-05; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zebrafish.";

Cell Death Differ. 7:509-510(2000).

EMBL, AR731017; AAR66962.2; -.

RSSP, Q92934, IG5J.

ESIN; EDS-GENE-000616-1; bad.

SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                            08K316
09R756
09R766
09R769
09SSP5
09CR233
097407
047148
047148
047149
063960
062972
062972
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047152
047173
062990
062974
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047174
062983
062980
062981
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                                                                    01-OCT-2000 (TrEMBLEEL 15, 01-DEC-2001 (TrEMBLEEL 19, 01-OCT-2002 (TrEMBLEEL 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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  Query Match
Best Local Similarity
Matches 15; Conserv
  \begin{array}{c} \mathcal{M} \otimes \mathcal{
68
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Q8VJS3;
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Q919N2;
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ID Q6
AC Q6
    2919N2
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080415 mycobacteri
080016 mus musculu
080271 pyrobaculum
09050 arabidopsis
09051 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9i9n2 brachydanio
                                                                                                                                                                                (without alignments)
237.680 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         September 15, 2003, 17:17:31 ; Search time 28.2286 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                           830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                       138
1 NLWAAQRYGRELRRMSDEFEGSFKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               summaries
                                                                                                                   using sw model
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010843
010843
08ZY71
09SZC0
09SQ22
09SQ17
09SQ17
09SQ17
08LB79
09SQ16
09SQ16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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Maximum Match 100%
Listing first 45 su
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sp_mhc:*
sp_organelle:*
sp_phage:*
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1: sp_archea:*
2: sp_bacteria:*
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sp_rodent:*
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Match
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Gaps

887 833 831 831 831 831 831 831 831 831

Result М М  $^{\circ}$ 

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946 AA
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5; Mismatches
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                              Created)
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SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
ij
                                         17
                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                          1 NLWAAQRYGRELRRMSD
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 34.6
Matches 9; Conservative
 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrobaculum aerophilum.
                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aerophilum.'
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                   Q8K016
Q8K016;
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 Matches
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                                                                                          RESULT .
Q8K016
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MEDLINE-9825987; PubMed-9634230;
MEDLINE-9825987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Esthan D., Brown D., Chillingworth T., Connor R., Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin M., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Stalton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the blology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Blishal W.;
Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Actinobacteria, Attinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBL_TaxID-1773,
                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 223;
                                                                                                                                                                                                                                                                                                                                        38.4%; Score 53; DB 16; Length 196; 58.8%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete protecme.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
                                                                                                                                                                                                                                                                                    InterProf. TRR003346; Transposase_20.
Pfan; PF02371; Transposase_20; 1.
SEQUENCE 196 AA; 21349 MW; C145A8D836FD9C2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv2014.
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 16;
Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natúre 393:537-544(1998).
-!- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 AA.
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Pfam; PF02371; Transposase_20; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     134 NLWAADRYNRAIARGHD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.4%;
                                                                                                                                                                                                                                                                                                                                                                                             1 NLWAAQRYGRELRRMSD 17
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01-WAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                        IS1607, transposase.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                          TIGR; MT2070;
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Q10843
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
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Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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  Indels
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034341; AAH34341.1; -.
EMBL; RG059619; Ithlo.
InterPro; IPR005687; VIT.
InterPro; IPR002035; VWE_A.
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EMBL: AE009793; AAL63125.1; -.
InterPro: JRP006688; Elp3.
InterPro: JRP00182; GGN3acetyltransf.

Pfam: PF00583; Acetyltransf; 1.

Pfam: PR00129; Elp3. 1.

Hypothetical protein, complete protecome.

SEQUENCE 471 AA, 52952 WW; 3B1E36E8AEE2EF0A CRC64;
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NCBL_TaxID=13773;
                                                                                                                                                                                                                                                                                                                    ol-War-2002 (TrEMBLrel. 22, Last sequence update) 01-Mar-2003 (TrEMBLrel. 23, Last annotation update) Inter-alpha trypsin inhibitor, heavy chain 2. IIIH2.
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01-MAR-2002 (TIEMBLED. 20, Last sequence update)
01-MAR-2003 (TIEMBLED. 23, Last annotation update)
Hypothetical protein PAE0922.
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS50066; MADS_BOX_2; 1.

DNA-binding; Nuclear Aptein; Transcription. Transcription regulation. SEQUENCE 23 AA, 27342 kW; BDFDCBS9973F4601 CRC64;
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Bubryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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MEDILINE-SO1284-49; PubMed=9927474;

MEDILINE-991284-49; PubMed=9927474;

Purugganan M.D., Suddith J.I.;

"Molecular population genetics of floral homeotic loci. Departures

from the equilibrium-neutral model at the APETALA3 and PISTILLATA

genes of Arabidopsis thallana.";

Genetics 151:839-848(1999).
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-!- SIMILARITY: BELONGS TO THE MADS DOWAIN FAMILY OF TRANSCRIPTION
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thallana."; Genetics 15:1839-848(1999).
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-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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ed. No. 18;
Mismatches 4; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; Pred. No. 1
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INTER_PO. IPR002487; TF_Kbox.
INTER_PO.; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00444; MADSDOMAIN.
SMART; SM00432; MADS, 1.
                                                                                                                                                                                                   EMBL; AF115806; AAD51895.1; -.
HSSP; P1746; 1MNM.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
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Best Local Similarity 44.4
Matches 12; Conservative
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Best Local Similarity 44.4
Matches 12; Conservative
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PROSITE; PS50066; MADS_DOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
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Makaryota, Varidiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SINILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99406148; PubMed=10474900;
Lavton Reulh A.L., Buckler E.S. IV, Purugganan M.D.;
"Patterns of molecular evolution among paralogous floral homeotic
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Pred. No. 18;
     DB 17; Length 471;
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                                                              11; Indels
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Last annotation update)
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01-MAY-2000 (TremBirel. 13, Last sequence update)
01-MAR-2003 (TremBirel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                      231 AA.
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                                                              3; Mismatches
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     37.7%; Score 52;
41.7%; Pred. No. 3
                                                                                                                                                      404 WQHSGMGREIMRLAEEIAGEFGAL 427
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                                                                                                                      3 WAAQRYGRELRRMSDEFEGSFKGL 26
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MEDLINE-99126449; PubMed-9927474;
Purugganan M.D., Suddith J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam: PF01486; K-box; 1.
Pfam: PF00319; SRF-TF; 1.
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HSSP; P11746; 1MNM.
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                                                              10; Conservative
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Arabidopsis lyrata.
  Query Match
Best Local Similarity
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PRINTS; PRO0404; MADSDOMAIN.
SURRT; SM00432; MADS; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription. SEQUENCE 232 AA; 27311 MW; 71AE593FB8A67EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Eagermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS50006; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SEQUENCE 232 AA, 27286 MW; 66976305B8B63E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes of Arabidopsis thallana.";
Genetics 15:1899-848(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                       Score 51; DB 10; Length 232;
Pred. No. 18;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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MEDLINE=99126449; PubMed=9927474;
                                                                                         EMBL. AF115807, AAD51896.1; -.
HSSP, P11746; IMNM.
InterPro; IPR002487; TF KDOX.
InterPro; IPR002100; TF_MADSDOX.
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InterPro; IPR002100; TF_MADSbox.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                           37.0%;
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Matches 12; Conservative
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Pfam; PF00319; SRF-TF; 1
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es 12; Conserv
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Best Local S:
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription, Transcription regulation.
SEQUENCE 232 AA; 27284 MW; 04FCFC55B73C7729 CRC64;
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Lisse;
MEDLINE-99126449; PubMed=9927474;
Purugganan M.D., Suddith J.I.;
"Modecular population genetics of floral homeotic loci. Departures
from the equilibrium-neutral model at the APETALA3 and PISTILLATA
genes of Arabidopsis thaliana.";
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MEDLINE-99156449; PubMed-9927474;
Purugganan M.D., Suddith J.L.;
"Molecular population genetics of floral homeotic loci. Departures
from the equilibrium-neutral model at the APETALA3 and PISTILLATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics 151:839-848(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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Pred. No. 18;
3; Mismatches 4; Indels
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Last annotation update)
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01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                                                                                             232 AA.
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               107 ORLGECIDELDIQELRRLEDEMENTFK 133
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PRT;
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InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; Kr Dox; I.
Pfam; PF00319; SRR-TF; I.
PRINTS; PR00404; MADSDOMAIN.
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les 12; Conservative
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FACTORS

Query Match

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SMART, SM0432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription, Transcription regulation.
SEQUENCE 232 AA; 27300 MW; 5CA05FD44F824DF0 CRC64;
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SEQUENCE 232 AA; 27314 MW; DB8CAIFC835557D6 CRC64;
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Wastyota, Wiidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Molecular population genetics of floral homeotic loci. Departures from the equilibrium neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
Genetics 15:1839-848(1999).
-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE MADS DOMAIN PAMILY OF TRANSCRIPTION
Genetics 151:839-848(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
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Pred. No. 18;
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InterPro; IPR002487; TE_Kbox.
InterPro; IPR002100; TE_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-FF; 1.
PRINTS; PR00404; MADSDOMAIN.
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MEDLINE=99126449; PubMed=9927474;
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SMARY; SW00432; MADS; 1.
PROSITE; PS00350; MADS, BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                 EMBL; AF115810; AAD51899.1; -.
HSSP; P11746; 1MNM.
InterPro; IPR002487; TE_Kbox.
InterPro; IPR002100; TE_MADSbox.
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44.4%;
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Matches 12; Conservative
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Pfam; PF00319; SRF-TF; 1
                                                                                                                                                                                                                                                                                                               232 AA;
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PROSTIE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27339 MW; CC90703F959CRAD5 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                           Floral homeotic protein APETALAS (APS).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
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MEDLINE=99126449; PubMed=9927474;
Purugganan M.D., Suddith J.L.;
"Molecular population genetics of filoral homeotic loci. Departures
from the equilibrium-neutral model at the APETALA3 and PISTILLATA
genes of Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.
Feldmann K.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                                                                                                           Last sequence update)
Last annotation update)
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18;
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InterPro; IPR002100; TE_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
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                                                                                                    01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 44.4*,
...has 12; Conservative
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 2.7340 WM; 6690703F9F9CED63 CRC64;
                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-99126449, PubMed=9927474;

Purugganan M.D., Suddith J.I.;

Purugganan M.D., Suddith J.I.;

Purugganan M.D., Suddith J.I.;

Purugganan M.D., Suddith J.I.;

Foreilar population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";

Genetics 15:1839-648(1999).

-- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
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                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                   232 AA.
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Arabidopsis thaliana (Mouse-ear cress).
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                                   PRT;
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EMBL; AF115799; AAD51887.1; --
HSSP; P11746; 1MMM.
InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF01486; K-box; 1.
Pfam; PF00449; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                 PRELIMINARY;
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RESULT 15
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Human Bad peptide
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BBC6 gene; cell death; cell cycle; Bcl2; human.
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AAU78620
AAU78624
ABG78485
ABG78492
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AAU78619
ABG78491
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AAU78618
AAU78625
AAU78628
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AAB70371
ABG78487
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AAU78629
ABG78496
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ABG78493
ABG78497
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AAU78615
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  96US-0665617.
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N-PSDB; AAT91561.
                                                                           \begin{array}{c} 8.3 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.9 \ 8.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \ 9.0 \
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Human Bcl-xL/Bcl-2
Human cell prolife
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                                                                                                                                                                           September 23, 2003, 09:43:16; Search time 86 Seconds (without alignments) 49.833 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  US-09-544-664B-2
142
14.2
1 NIVAAAĞİYELIRRMSDEYUDSFKKGL 27
1 NIVAQQİY (1010) ŞPRIN DAR DARA XAZI
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Maximum Match 100%
Listing first 45 summaries
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AAB13512
AAB70368
AAB48287
AAG67688
ABR39081
ABP41630
ABP56161
                                                                                                                           using sw model
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Match 1
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116:
116:
120:
221:
23:
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Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Mutant Bcl2 compet Human Bad peptide Human Bad peptide Mutant Bcl2 compet

Human Bad peptide Bcl2 polypeptide B Bcl2 polypeptide B Bcl2 polypeptide B

Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bc1-2

Human ovarian anti PTPC-interacting T

Score

Result МО. 137 137 137 137 137 137 127

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detection and diagnosis,
                             168 AA;
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                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                  02-NOV-2000
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                              Sequence
                                                                                                                                                                                                                        AAB13512;
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Matches
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AAB13512
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                        The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with BC1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-xI results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as cancers, e.g. lymphoma and hormone dependent tumours, autoimmune diseases, e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis and viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad can also be used for
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                               Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad; programmed cell death; apoptosis.
                                                                                                                                                                                               ;
                                                                                                                                                                     Length 166;
                                                                                                                                                                                                                                                                                                                                                                                    Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
                                                                                                                                                                                               Indels
                                                                                                                                                                                   1.le-12;
                                                                                                                                                                    Score 137; -- DB-18;
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0; Mismatches
                                                                                                                                                                                                                                   101 NLWAAQRYGRELRRMSDEFVDSFKKGL 127
                                                                                                                                                                                                         1 NEWAAGEGGELRRMSDEFVDSFKKGL 27
Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                            AAW55779 standard; Protein; 168 AA.
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                                                                                                                                                                  96.5%;
ilarity 96.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IDUN-) IDUN PHARM INC.
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                           166 AA;
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AAW55779
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shares structural and chemical homology with Bol-2, is involved in cell proliferation. Its coding sequence was isolated by screening a synovial proliferation. Its coding sequence was isolated by screening a synovial alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated inflammation such as Addison's atherness syndrome, allergies, ansemia, asthma, atherosolerosis, Crohn's disease, ulcrative colitis, disbetes mellitus, emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, rheumatoid arthritis, Sjogram's syndrome and autoimmune thyroiditis, complications of cancer, haemodialysis and extracoxporeal circulation, infections, trauma, disorders with associated apoptosis including AIDs and other infectious and genetic immunodeficiencies, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, ischeemic injuries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with cell proliferation for diagnosis, prevention and treatment of e.g. cancer, acquired immunodeficiency syndrome, and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as myocardial infarction, and wasting diseases including cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide and polypeptide sequences of proteins associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the human APOP-1 protein. This protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cell proliferation; APOP-1; cancer; inflammation; infection;
trauma; neurodegenerative disease; ischaemic injury; wasting disease.
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   Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.5%; Score 137; DB 23; 96.3%; Pred. No. 1.1e-12; ive 0; Mismatches 1;
Score 137; DB 19;
Pred No. 1.1e-12;
                                                                Mismatches
                                                                                                                                                              103 NIWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cell proliferation protein APOP-1
                                                                                                                       1 NLWAAQEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lal
                                                                                                                                                                                                                                                                                                                                            AAB13512 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
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   96.5%;
96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0985335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-451230/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 26; Conserv
                         Local Similarity
es 26; Conserv
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RESULT 6
                                                                                                                                                 RESULT 5
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                                                                                                                                                                                AAB48287
                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bel-XL/Bel-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser118 of a human BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a human BAD (serification acid substitutions at Ser113 of a murine BAD) antiarthe BAD). (I) has immunosuppressive activities, and contropic, antiinflammatory and immunosuppressive activities, and antiarthritic, antiinflammatory and immunosuppressive activities, and polypucial inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include indentified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attinium and attin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; mumuostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiancy disease; neurodegenerative disease; viral infection; isobaemic cell death; reperfusion cell death; arthritis; infection; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BAD mutant amino acid sequence SEQ ID NO:1.
                                         103 NIWAAQRYGRELRRMSDEFVDSFKKGL 129
      27
1 NIWAAQEYGRELRRMSDEFVDSFKKGL
                                                                                                                                                                                                                                    AAB70368 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 147; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000WO-US11864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0136783
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                         AAB70368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou X;
                                                                                                                                                                                                     AAB70368
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The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                           S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bcl-2; tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cell proliferation; APOP-1; APOP-2; APOP-3; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of protein associated with cell proliferation-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168;
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NEWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NLWAAQENGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 102-103; 162pp; English.
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                                                                                                                                   standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG67688 standard; Protein; 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2000; 2000WO-US15449.
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                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsvetkov LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-061703/07.
N-PSDB; AAC84599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 AA;
                                                                                                                                                                                                                                                                    Human Bad protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200075184-A1.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1999;
                                                                                                                                                                                                                        02-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang H,
                                                                                                                              AAB48287
                                                                                                                                                                            AAB48287;
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0;

Gaps

0

Length 168; **Undels** 

Score 137; DB 22; Pred. No. 1 1e-12; 0; Mismatches

96.5%;

Query Match
Best Local Similarity 96.33
Matches 26; Conservative

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Human, ovarian antigen, ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pcCoS; ovarian cyst; dysmeorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method (MI) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptoit oplypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 166 residue amino acid sequence (see ABR39081), where the peptide comprises seril2, ser135, or ser155, or their combinations. BAD has virucide activity. MI is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 is useful for treating a patient infected with HSV with HSV. The present sequence represents human BAD, which is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducing apoptosis in a cell infected with herpes simplex virus, ESV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                   Human; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 137; DB 24;
Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian antigen HCE4K28, SEQ ID NO:2762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 166-167; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP41630 standard; Protein; 201 AA.
    Human BAD protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.5%;
                                                                                                                                                                                                                                                  31-JUL-2002; 2002WO-US24177.
                                                                                                                                                                                                                                                                                            31-JUL-2001; 2001US-308929P.
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                                                                                                                                                                                                                                                                                                                                                                                  Munger J, Roizman B;
                                                                                                                                                                                                                                                                                                                                        (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-248168/24.
                                                                          virucide; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABZ81200.
                                                                                                                                                            WO2003012049-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Sim. 26;
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2002
                                                                                                                                                                                                      13-FEB-2003
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      Q
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                                                                                                                                  10..13
/note= "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                 /note= "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                            /note= "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                              /note= "potential protein kinase C phosphorylation site"
153..156
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "potential casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human protein which is associated with cell proliferation, designated APOP-1. The specification also describes APOP-2 and APOP-2. The APOP polypeptides are useful for diagnosing, preventing or treating disorders associated with abnormal cell proliferation and apoptosis. The polypeptides and composition are particularly useful for treating or preventing cancer (e.g. brain or breast cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease or Parkinson's disease) or inflammation (e.g. allergies, gout, osteoarthritis or bronchitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides associated with cell proliferation, useful for preventing or treating cancer (e.g. brain cancer), a disorder associated with an increase in apoptosis (e.g. Alzheimer's disease) or
brain cancer; breast cancer; Alzheimer's disease; Parkinson's disease; inflammation; allergy; gout; osteoarthritis; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                             /note= "potential protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                    /note= "potential cAMP- and cGMP-dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.5%; Score 137; DB 22; Length 168; 96.3%; Pred. No. 1.1e-12; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corley NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQEKGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shah P,
                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 1A-C; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR39081 standard; Protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0410372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0985335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                              124..126
                                                                                                                                                                                                                                                                                                               115..118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation (e.g. gout)
                                                                                                                                                                                                                           34..36
                                                                                                                                                                                                                                                                       80..83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-569961/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH78430.
                                                                                                               Key
Modified-site
                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2003
                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6281334-B1
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Gaps

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Sequence

Query Match

ABR39081;

AXXXXXXXXXXXX

RESULT 7 **ABR39081** 

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Length 168; Indels

WO200200677-A1. Homo sapiens.

03-JAN-2002.

N-PSDB; ABQ54707

Birse CE,

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of the mitochondia of its fragment. (1) has virucide, neuroprotective, vasotropic and cytostatic activities, and can be used as a mitochondrial permeability transition proce complex (PPPC) modulator. (1) is useful for treating or preventing a pathological infection or disease. (1) is also useful for regulating cell death regulatory modecules, specifically the apoptogenic function of the PTPC, for treating e.g. cancer, isothaemia, neurodegenerative diseases, fulminant hepatitis or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a chimeric bifunctional molecule (I) comprising at least a first functional molecule covalently linked to a second functional molecule, which is able to modulate the activity of the permeability transition pore complex (PPPC) of the mitochondria. (I) has the function of specifically targeting and entering a tissue celli population. The second functional molecule has the function of specifically targeting, and inducing or preventing the death of the cells by apoptosis by regulating the opening or the closing of the PPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a PTPC-interacting TOX peptide which is given in the exemplification of the present invention.
                                                                                                                                                                                                         apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                  permeability transition pore complex; virucide; neuroprotective; vasotropic; cytostatic; infection; cell death regulation; apoptosis; mitochondrial permeability transition pore complex modulator; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric bifunctional molecules that target specific cells and regulate the apotosis function of the permeability transition pore complex of the mitochondria, useful for treating or preventing e.g. cancer or ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                   Mitochondrial membrane permeabilisation; mitochondrion; PTPC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.4%; Score 127; DB 23; 96.0%; Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred No. 4.26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG78484 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Briand J;
                               PTPC-interacting TOX peptide #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 11; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2001; 2001US-265594P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edelman L, Jacotot E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-619260/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AA;
                                                                                                                                                                                                                                                                                                                            WO200261105-A2.
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                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-2002
                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating, prognosing or preventions our polypeptices in displaced.

Treating, prognosing or preventing various ovarian in displaced.

Glisorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system clisorders (e.g., infertility, disorders of pregnancy, anovulation.

Delyoystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertings (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and variant cysts and disorders (e.g., congenital and acquired them to a spiration disorders (e.g., congenital and acquired disorders, authimmune Ophoritis, systemic lupus erythematosus), conditionates, authimmune cophoritis, systemic lupus erythematosus), conditionatory disorders (e.g., anomala), cardiovascular disorders and uninary system disorders (e.g., congenital polypeptides and conditionation of individuals and in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used to gene therapy, chromosome mapping, in the collection of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP43228) and to CDNAs encoding them (ABD54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodaes against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 2175 novel human ovarian antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID No 2762; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 NLWAAQRYGRELRRWSDEFVDSFKKGL 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.5%;
96.3%;
                                                                                                                                                                                                      07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                                                 07-JUN-2000; 2000US-209467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurological diseases
                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-147878/19.
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ABP56161;

SXX E

RESULT 9

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Sequence Query Match Matches H

Shang

Matayoshi E,

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Swift KM,
    Nettesheim DG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
ABG78490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel mutant protein which is derived from a wild type human BC1-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type BC1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant BC1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that the BC1-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of BC1-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human BC12 peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                     New mutant Bc1-2 proteins derived from a wild type human Bc1-2 protein, useful in biological assays to identify substances that block the ability of Bc1-2 to inhibit programmed cell death or apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Bad peptide #10 which binds to a member of the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.4%; Score 127; DB 23; 96.0%; Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                            Nettesheim DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 17; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä.
                                                                                                                                                                                                                                                                            Yoon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78610 standard; Peptide; 25
                                                                                                                                                         15-NOV-2001; 2001WO-US45693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2001; 2001WO-US27410.
                                                                                                                                                                                              20-NOV-2000; 2000US-0716395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000; 2000US-0656399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similaric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fesik SW, Meadows RP,
                                                                                                                                                                                                                                                                            Petros AM,
                                                                                                                                                                                                                                                                                                               WPI; 2002-490141/52.
                                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 AA;
                                                                            WO200240530-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200220568-A2
                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2002
                                                                                                                   23-MAY-2002
                                                                                                                                                                                                                                                                            Fesik SW,
                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU78610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
                                                                 New derivatives of Bad peptide, useful for identifying compounds that bind to Bcl-2 proteins, potential agents for treating cancer and degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant Bcl2 competitive binding assay peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nettesheim DG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127;
Pred. No. 4.
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                                                                                                                                                                                                             Claim 18; Page 18; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petros AM,
WPI; 2002-292254/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-490141/52.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB.
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NLWAAQEYGRELRRMSDEFVDSFKK 25
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                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                           15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2002.
                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                            ABG78488;
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                                                                                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to potentially useful for treating anner (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein substances of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2 peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss of Bad peptide, useful for identifying compounds that proteins, potential agents for treating cancer and
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Bad peptide #17 which binds to a member of the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                          Length 25;
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Pred. No. 1.2e-11;
1; Mismatches 1; Indels
                                                                                                                                                                     Score 124; DB 23; Length 2
Pred. No. 1.2e-11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ows RP, Joseph MK, Olejniczak ET,
Swift KM, Matayoshi E, Zhang H;
                                                                                                                                                                                                                                           1 NLWAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                          1 NIWAAORYGRELRRMSDEFVDAFKK 25
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                                                                                                                                                                                                                                                                                                                                                           AAU78617 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New derivatives of Bad peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.3%;
                                                                                                                                                                        87.3%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2001; 2001WO-US27410.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                   Query Match
Best Local Similarity 92.0°
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.3
Best Local Similarity 92.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       degenerative disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AA;
                                                                                                                                        25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200220568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bind to Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fesik SW,
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                             RESULT 13
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HANDER DE STANDER DE S

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This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type BC1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant BC1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the BC1-2 protein. The protein squences of the invention are useful in biological assays to identify substances that block the ability of BC1-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human BC12
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                         Mutant Bcl2 competitive binding assay peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant Bcl2 competitive binding assay peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 123; DB 23;
Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nettesheim DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
1 NEWAAQRYGRELRRMSDEFVDAFKK 25
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                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 17; 36pp; English.
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92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001; 2001WO-US45693.
                                                                                                                                                                                   ABG78488 standard; Peptide;
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Best Local Similarity 92.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petros AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-490141/52.
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                                                                                                                                                                                                                                                                                                                                                             New mutant BC1-2 proteins derived from a wild type human BC1-2 protein, useful in biological assays to identify substances that block the ability of BC1-2 to inhibit programmed cell death or apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                 Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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86.6%; Score 123; DB 23; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.7e-11;
Matches 23; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                             Yoon H, Nettesheim DG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 17; 36pp; English
                                                                                                                                                                                    15-NOV-2001; 2001WO-US45693
                                                                                                                                                                                                                     20-NOV-2000; 2000US-0716395
                                                                                                                                                                                                                                                                                             Fesik SW, Petros AM,
                                                                                                                                                                                                                                                                                                                                  WPI; 2002-490141/52
                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB
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                                                                                                           WO200240530-A2.
                                                     Homo sapiens.
Synthetic.
                                                                                                                                               23-MAY-2002
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Search completed: September 23, 2003, 09:47:13 Job time : 87 secs

1 NLWAGQRYGRELRRMSDEFVDSFKK 25

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Sequence 40, Appl Sequence 56, Appl Sequence 20008, Appl Sequence 2, Appli Sequence 2710, Ap Sequence 1058, Ap Sequence 6559, Ap Sequence 6559, Ap

US-09-252-991A-26276
US-09-252-991A-17508
US-09-352-991A-17508
US-08-379-556A-2
US-08-379-556A-2
US-08-379-532-56
US-09-511-451-56
US-09-252-991A-20008
US-09-147-923-2
US-09-147-923-2
US-09-147-923-2
US-09-328-352-710
US-09-328-352-74058
US-09-328-352-74058
US-09-328-352-74058
US-09-328-352-74058
US-09-328-352-74058
US-09-328-352-74058

23461,

Sequence 10, 8 Sequence 23461 Sequence

US-09-091-501B-8 US-09-091-501B-10 US-09-252-991A-23461 US-08-261-660A-17

Sequence 17508, A Sequence 18296, A Sequence 2, Appli

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Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                              September 23, 2003, 09:43:16 ; Search time 30 Seconds
    (without alignments)
38.080 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-985-335-1
US-08-986-335-1
US-09-410-372-1
US-09-410-372-7
US-09-375-25-2
US-08-33-565-2
US-08-61-479-2
US-08-733-505A-1
US-08-733-505A-13
US-08-733-505A-13
US-08-733-505A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                              US-09-544-664B-2
142
1 NLWAAQEYGRELRRMSDEFVDSFKKGL/27
                                                                                                                                                                                                                                                                                                                                                                                           328717 segs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                     Run on:
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Sequence 2, Application US/08665617

Patent No. 566316

GENERAL INFORMATION:

APPLICANT: Xudong, Yin

TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2

CORRESPONDERCE ADIAMANCH & Saliwanchik
STREET: 2421.N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,617 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.38
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.5%; Score 137; 96.3%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 NIWAAQRKGRELRRWSDEFVDSFKKGL 127
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                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanohik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 01.
TELEPONNUNICATION INFORMATION:
TELEPONE: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.35
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-665-617-2
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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US-08-665-617-2
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RESULT 2

Sequence 26, Appl Sequence 34, Appl Sequence 69, Appl Sequence 69, Appl Sequence 18729, A

US-08-924-695A-69 US-09-252-991A-18729

Sequence 1, A Sequence 12, Sequence 13, Sequence 14,

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

US-08-717-123-3 US-08-717-123-3 US-08-315-257-3 US-08-661-479-10 US-08-733-505A-55 US-08-733-505A-55 US-08-733-505A-57 US-08-733-505A-57 US-08-733-505A-57 US-08-733-505A-54 US-08-733-505A-34 US-08-733-505A-34 US-08-733-505A-34 US-08-733-505A-34 US-08-733-505A-34 US-08-733-505A-34

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Length 168;
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Lat, Preet,
APPLICANT: Corley, Neet,
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
         FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%; Score 137; DE cilarity 96.3%; Pred No. 5.46 Conservative 0; (Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
      SOFTWARE: FASTER, NO. CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPHONE: 650-855-055
TELEPHONE: 650-855-055
TELEPHONE: 650-855-055
TELEPHONE: 650-855-055
TELENGTH: 168 amino acids
STOURNE amino acid
STOPOLOGY: linear
TYPE: amino acid
STOPOLOGY: linear
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APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-985-335-7; Sequence 7, Application US/08985335; Patent No. 6080847
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REGISTRAILON NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPRINGE: 650-845-165
INFORMATION FOR SEQ ID NO: 7:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Porter Dr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: SYNORAB01
CLONE: 358673
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Best Local Similarity
Matches 26; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 35-1
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                                                                                 GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 168;
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEB: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STREE: CA
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FURE:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNGRER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SSS 935-9001
TELECOMMUNICATION SSS 1000:
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TELECOMMUNICATION OF SSS 10
                                                                                                                                                                                                                                                                                       ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.5%; Score 137; DB 2; 96.3%; Pred, No. 5.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.-5.4e
0; Mismatches
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                        Sequence 2, Application US/08717123
Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
COUNTY: United States
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.5
Best Local Similarity 96.3
Matches 26; Conservative
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US-08-717-123-2
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SEQUENCE CHARACTERISTICS

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Sequence 2, Application US/09375257

Parent No. 6504022

GENERAL INFORMATION:
APPLICANT: HORNE, William A.
APPLICANT: Oltersdorf, Tilman; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC; TITLE OF INVENTION: ACIDS AND METHODS OF USE; FILE REPERRANCE: 480140.42801

CURRENT APPLICATION NUMBER: US/09/375,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tength 168;
                                                                                                                                            GENERAL INCRMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLEFRATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARES: FactSEE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
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96.3%; Pred No. 5,4e-
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
103 NLWAAQRYGRELRRMSDEFVDSFKKGL 129
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APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                           Sequence 7, Application US/09410372
Patent No. 6281334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO:
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: US,
ZIP: 94304
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                                                                                           US-09-410-372-7
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GENERAL INPORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Tal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Carley, Neil, C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                    Score 137; DB 3; Le
Pred No. 5.48-14;
0: Mismatches 1;)
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96.3%; Pred_No.-5.4e-14;
tive 0; Mismatches 1;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                               1 NIWAAQEYGRELRRMSDEFVDSFKKGL 27
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FILING DATE:
ATOANET/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
""" FPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
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                                                                                                                                                                                      96.5%;
96.3%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
             LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ILMBELRARS SOURCE:
LIBRARY: Genbank
CLONE: 1683637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 168 amino acids
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Best Local Similarity 96.3
Matches 26; Conservative
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Matches 26; Conservative
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STRANDEDNESS: si
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LIBRARY: Sinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.8%; Score 109; DB 2; Length 204; 87.5%; Pred. No. 1.7e-09;
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                                                                                             GENERAL INFORMATION:
APPLICANT: KORSMETER, Stanley J.
IITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGGLATOR
                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto CITY: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PR PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-UN-1995
CLASSIFICATION: 433
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATORNEY/AGENT INFORMATION:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 15726A-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
ITELEPHONE: (415) 326-2400
ITELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                 US-08-661-479-2
; Sequence 2, Application US/08661479
; Patent No. 5834209
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                                                                                                                                                                                             NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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Matches 21; Conserv
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STATE: MISSOURI
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Sequence 2, Application US/08333565

Patent No. 5622852

GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCJ-x/Bcj-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Deduced amino acid sequence of mouse BAD."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIE PC-DOS/MS-DOS
SOFTWARE: PATCHIE PC-DOS/MS-DOS
SOFTWARE: PATCHIE BC-DOS/MS-DOS
SOFTWARE: PATCHIE BC-DOS/MS-DOS
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: SMITC, WILLIAM M
REGISTRATION NUMBER: 15726A-000700
TRIEDCOMMUNICATION INFORMATION:
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TRIEDCOMMUNICATION OF 2:
SEQUENCE:
LENGTH: 204 amino actids
LENGTH: 204 amino actids
                                                                                                                                                                                                                                                                0; Mismatches
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                          103 NIWAAQRGRELRRMSDEFVDSFKKGL 129
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Best Local Similarity 87.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-257-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
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                                                                                                                                                                                                                                     Best Local Similarity
Matches 26; Conserv
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US-08-733-505A-14

Sequence 14, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:

APPLICANT: KORNEYER, STANLEY J.

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

TITLE OF ENVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

TITLE OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
UNDRER OF SEQUENCES: 60
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                                                                    Length 204;
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                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                               Query Match 76.8%; Score 109; DB 2; Best Local Similarity 87.5%; Pred. No. 1.7e-09; Matches 21; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 NLWAAQRYGRELRRMSDEFEGSFK 163
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                                                                                                                                                                 1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08733505A; Patent No. 585645; GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERRNCE/DOCKET NUMBER: 9654.
TELECOMMUNICATION INFORMATION:
TELEPRAX: (314) 727-5188
TELEPRAX: (314) 727-6182
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 204 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
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US-08-733-505A-13
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APPLICANT: KORSMEYER, STANLEY J.

APPLICANT: KORSMEYER, STANLEY J.

TILLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BCL.*XL/BCL.^2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFFRKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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ZIE: 63105

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRB PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                               APPLICATION NUMBER: US/08/733,505A FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: (314) 727-5188
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-6092
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOTOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERRANCE/DOCKET NUMBER: 9654;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPRONE: (314) 727-5188
TELEPRAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGRET INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5'
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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US-08-733-505A-12
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TYPE: PRT
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Sequence 3, Application US/08717123

Sequence 3, Application US/08717123

Fatent No. 5965703

GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic

TITLE OF INVENTION: Acids and Methods of Use

NUMBER OF SEQUENCES: 15

CORRESPONDENCES: 15

CORRESPONDENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego.

CITY: San Diego.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.8%; Score 109; DB 2; Length 204; Best Local Similarity 87.5%; Pred. No. 1.7e-09; Matches 21; Conservative 0; Mismatches 3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/117,123
FILING DATE: 20-25P-1996
CLASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathry A.
REGISTRATION NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8001
TELEPHONE: (619) 535-8049
; INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
: 7733 FORSYTH BLVD., SUITE 1400
ST. LOUIS
MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILLNO DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INCOMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
ANA MAIN A ACID SECOND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NIWAAQRYGRELRRMSDEFEGSFĶ 163
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                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                 63105
                                                                                           STATE: M
COUNTRY:
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Patent No. 6504022

GENEBAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: HOMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140,428nl
CURRENT APPLICATION NUMBER: US/09/375,257

CURRENT PILING DATE: 1999-08-16

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 204
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Best Local Similarity 83.3%; Pred. No. 5e-09;
Matches 20; Conservative 1; Mismatches 3; Indels
                                                                                                                                      Score 106; DB 2; Length 204;
Pred. No. 5e-09;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                  1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                        Query Match 74.6%;
Best Local Similarity 83.3%;
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus
US-09-375-257-3
                                                                                                                                                                                                                                                                                                                                                                      US-09-375-257-3
                                                                                          US-08-717-123-3
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September 23, 2003, 09:47:20; Search time 389 Seconds (without alignments) 10.335 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.puB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.puB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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142
1 NLWAAQEYGRELRRMSDEFVDSFKKGL 27
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 1, Application US/09894657 Patent No. US20020098559A1 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L.

RESULT 2 US-09-894-657-1 Yue, Henry Lal, Preeti Shah, Purvi

4424, App 141, App 1, A	40
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Gaps
Sequence Seq	υ ;; 
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	16 1.8
4 60 84 E	C H
2-13424 444-8 70-241 70-810 70-810 861-1099 861-1099 86-11148 86-1	S, ENCODING USE USE DB 9; Lee DB 9; Lee 12.
2222426 22222426 222226 222226 222236 222	
US-09-815-242-13424 US-10-092-750-241 US-10-342-24-110 US-10-323-070-8 US-10-223-070-8 US-10-125-761-10995 US-10-156-761-10995 US-10-156-761-10995 US-10-156-761-110995 US-10-136-761-110995 US-10-136-761-110995 US-10-234-432-37 US-10-234-432-37 US-10-124-432-37 US-10-124-432-38 US-09-815-242-10793 US-09-815-242-10793 US-09-815-242-10793 US-10-140-018-218 US-10-140-924-218 US-10-140-926-218 US-10-140-926-218 US-10-140-926-218 US-10-140-926-218 US-10-141-704-218	ALILYPE LYPE ETHO 9/92 rsio red. Mi SFKK
	US/09922378 A1 Tilman Tilman A2N BAD POLJ 1DS AND MET 428D3 BER: US/09, 001-08-03 5 10dows Vers 1100ws Vers
       	ion US/0992 87869A1 1111am A. Norf, Tilman 1140.42BD3 1140.42BD3 1140.42BD3 NUMBER: US 1201.08-201.08-201.08-38: 2. 2001.08-38: 2. 201.08-38: 3. 201.08-38: 3. 1201.08-38: 4. 96.38: 5. 1201.08-38:
25.55 25.25	ALIGNM  APPLICATION US/09922378 US20020037869A1 US20020037869A1 US20020037869A1 Oltersdorf, Tilman Oltersdorf, Tilman NEWRINN: HUMAN BAD POLYPEPTI NYENTION: HOMOWER: US/09/922, 387 HOMO SAPIENS SAPIENT HOMO SAPIENS SAPIENT HOMO SAPIENS SAPIENT HOMOWER BAD SERVER HOMOWER BAD SERVER HUMANAQUERELRRMSDEFVDSFKKGL HILL
O O O O O O O II II II II II II II II II	-378-2  e 2, Applon. US200  INFORMAL  ANT: O11  ANT: O11  OF INVENT  OF INVENT  T FILLO  OF SEQ.  OF SEG.  OF S
UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	RESULT 1 Sequence 2, Application US/099223 Sequence 2, Application US/099223 Patent No. US20020037869A1 GENERAL INFORMATION: APPLICANT: HOTNE, William A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: HUMAN BAD FOT INTLE OF INVENTION: ACCES AND M. FILE REFERENCE: 480140.428D3 CURRENT APPLICATION NUMBER: US/0 CURRENT APPLICATION NUMBER: US/0 CURRENT APPLICATION NUMBER: US/0 CURRENT APPLICATION NUMBER: US/0 CURRENT APPLICATION NUMBER: US/0 CURRENT APPLE: PRT OGNERAL FOR US/0 I EMOTH: 168 TYPE: PRT US-09-922-378-2 OUGLY MATCH  OUGLY MATCH  I NUMBAR/CRELREMSDEFVD  ON UNMARANCERERREMSDEFVD  DD  103 NUMBAR/CRELREMSDEFVD  DD  103 NUMBAR/CRELREMSDEFVD
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APPLICANT: MUNGER, JOSHUA
APPLICANT: MUNGER, JOSHUA
APPLICANT: ROIZMAN BERNARD
TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS
FILE REFERENCE: ARCD:38005
CURRENT APPLICATION NUMBER: US/10/209,967
CURRENT APPLICATION NUMBER: 06/308,929
PRIOR FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%; Score 137; DB 9; Length 168; 96.3%; Pred, No. 17.26-12; live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
      OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%; Score 137; DB-127, 96.3%; Pred No. 1.2e-12;
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: B1111045, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred No. 1.2e
                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28 - Un - 2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 NIWAAQRYGRELRRMSDEFVDSFKKGL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/10209967; Publication No. US20030171279A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.34
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: GenBank
CLONE: 1683637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human BAD
US-10-209-967-2
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US-10-066-179-2
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Tue, Henry
Ial, Preeti
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILLING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
COLLEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL.
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNION NUMBER: 09/410,372
FILING DATE: CUDKOWN
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 86,749
REFERENCE/POCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 168 amino acids TYPE: amino acid
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Patent No. US20020098569Al
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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IMMEDIATE SOURCE:
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Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                        COUNTRY: US
ZIP: 94304
                                                                                                                                                                       STATE: CA
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US-09-894-657-7
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US-10-066-179-3
Sequence 3, Application US/10066179
Sequence 3, Application US/10066179
Publication No. US20020115631A1
GENERAL INFORMATION:
APPLICANT: HORNEY WIlliam A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT APPLICATION NUMBER: US/10/066,179
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
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                                                                                                                                                                                               Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HOLORATION, William A.
APPLICANT: HOLORA WILLIAM A.
APPLICANT: OITERSOOF, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SEQ ID NOS: 15
SEQ ID NOS: 15
LENGTH: 204
                                                                                                                                                                                               Score 109; DB 12;
Pred. No. 2.1e-08;
0; Mismatches 3;
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Patent No. US20020037869A1
                                                                                                                                                                                                  Query Match 76.8%;
Best Local Similarity 87.5%;
Matches 21; Conservative
       NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Matches 20; Conservative
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Matches 20; Conservative
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US-10-066-179-3
                                                                                                    TYPE: PRT
CORGANISM: Mus musculus
US-10-209-967-4
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US-09-922-378-3
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                                                                                   LENGTH:
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Sequence 258, Application US/10059261
Sequence 258, Application US/10059261
Publication No. US20030077826A1
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: BDELMAN, LENA
APPLICANT: BUNGNYION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APPLICANT:
TITLE OF INVENTION: (PPPC)
TITLE OF INVENTION: (PPPC)
TITLE OF INVENTION: (PPPC)
TITLE OF INVENTION: (PPPC)
STIRE REGULATION OF THE PERMEABILITY TRANSITION PORE COMPLEX
CURRENT APPLICATION UNDER: US/10/059, 261
CURRENT FILING DATE: 2002-08-29
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Sequence 4, Application US/10209967
Publication No. US20030171279a1
GENERAL INFORMATION:
APPLICANT: MUNCER, JOSHUA
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND TITLE OF INVENTION: METHODS AND PRICE REFERENCE: ARCD:380US
CURRENT EPLICATION NUMBER: US/10/209,967
CURRENT FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                                                                         Query Match 96.5%; Score 137; DB 14; Length 168; Best Local Similarity 96.3%; Pred. No. 1.3e-12; Matches 26; Conservative 0; Mismatches 1; Indels
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
TILE REFERENCE: 480140.4238C1
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/265,594
PRIOR FILING DATE: 2001-02-02
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SEQ ID NO 258
LENGTH: 25
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-066-179-2
                                                                                                                                                                              SEQ ID NO 2
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US-10-209-967-4
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APPLICANT: Bhatia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: SKeiky Vesir A.W.
APPLICANT: PEOSE, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERRORS: 210121,46908
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT PELING DATE: 2001-04-23
NUMBER OF SEQ. ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.1%; Score 47; DB 11; Length 350; 40.9%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.7%; Score 46.5; DB 9; Best Local Similarity 40.7%; Pred. No. 2.3e+02; Matches 11; Conservative 7; Mismatches 6;
                                                                                                                                                    Sequence 394, Application US/09940244;
Publication No. US20030044796A1
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Mall, Jeff G.
APPLICANT: Main, Lloyd M.
TILLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 969 NLYLAQPDGKKLSNM---YLTAWKKGL 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 583, Application US/09841132 ; Patent No. US20020061848A1
6 QEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AAQEYGRELRRMSDEFVDSFKK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: C. Trachomatis D serovar
US-09-841-132-583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
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                                                                                                                                       US-09-940-244-394
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LENGTH: 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 394
LENGIH: 350
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                                                                           Sequence 147, Application US/10174105A; Sequence 147, Application US/10174105A; Publication No. US20030068652A1

SEQUENCE INFORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: COMB, Michael J.
APPLICANT: CAMB, Michael J.
APPLICANT: TAN, YI
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
TITLE OF INVENTION: US/10/174,105A
TITLE OF INVENTION: US/10/174,105A
CURRENT APPLICATION NUMBER: US/10/174,105A
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 193
SOFTWARE: PATCHING VERSION 3.1
SEQ ID NO 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10168780

Publication No. US20030172405A1

Septembal Involvative Nicolation US/10168780

Specification No. US20030172405A1

APPLICANT: TANKA, Nicolation APPLICANT: TANKA, Masatomo

APPLICANT: TANKA, Masatomo

APPLICANT: TANKA, Masatomo

APPLICANT: TANKA, Masatomo

APPLICANT: TANKA, Masatomo

APPLICANT: TANKA, Masatomo

APPLICANT: TANKA, Masatomo

APPLICANT: TANKA DATE: US/10/168,780

CURRENT FILING DATE: 2002-06-20

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 1999-12-20

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 2

LENGTHARR PARENT VAIL VAIL 2.0

SEQ ID NO 2

LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.1%; Score 57; DB 15; Length 15; 85.7%; Pred. No. 0.063; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GRELRRMSDEFVDS 22
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Matches 12; Conserv
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                                                                      US-10-174-105A-147
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US-10-168-780-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence. 100 4

Sequence. 100 4

Publication No. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Hammond, Philip W.

APPLICANT: Wright, Martin C.

TITLE REFERENCE: 50036/050002 100/092,750

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR PRIOR PAPER: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: RestSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 35

TYPE: PRI T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.4%; Score 46; DB 15; Length 35; Best Local Similarity 55.6%; Pred. No. 6.8; Matches 10; Conservative 2; Mismatches 2; Indels
APPLICANT: Probst, Peter TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT TITLEOF INVENTION: AND DAGGNOSIS OF CHLANTDIAL INFECTION FILE REFERENCE: 210121.515C2
CURRENT APPLICATION NUMBER: US/10/007,693
NUMBER OF SEQ ID NOS: 157
LENGTH: 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 23, 2003, 10:03:35 Job time : 390 secs
                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Chlamydia trachomatis serovar D US-10-007-693-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                  969 NLYLAQPDGKKLSNM---YLTAWKKGL 992
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15 IWIAQ----ELRRIGDEF 28
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US-10-092-750-1
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US-10-092-750-1
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September 23, 2003, 09:43:16; Search time 22 Seconds (without alignments) 57.715 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                           US-09-544-664B-2
142
1 NIWAAQEYGREIRRMSDEFVDSFKKGL 27
                                                                                                                                                                                                                                                                                                                                   127863 seqs, 47026705 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q92934 homo sap	Q61337 mus m	035147	013049	P09915	Q8r943		Q9veb3		L P79023	P30209	033925	P43086	064206	P52323	Q8k2h3	Q8evw9	066853	Q9p193	084834	043521	Q9zcy2	Q075 <u>1</u> 2	E Q9yci2 aeropyr	P12436	Т р38198	BACSU P42103 bacillus	. ,		058413	$\sim$	
1		ឧ	BAD_HUMAN	BAD_MOUSE	BAD_RAT	HT2A_HUMAN	MTBR_BPRH	PPCK_THETN	AROG_YEAST	BXD1_DROME	HXK_DEBOC	AROG_CANAL	VP5_BTV2A	SYM_THEMA	PPCK_RHISN	VG13_BPMD2	RPSD_BORBU	CE05_MOUSE	IPYR_MYCPE	Y591_AQUAE	RIR1_CHI	RIR1_CHLTR	BIM_HUMAN	MRAW_RICPR	FLS_PETHY	TNAA_AERPE	VP5_BTV1A	STU1_YEAST	XXAD_BAC	PPCK_BAC	- 1	SYV_METUR	- 1	
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	•	Match Length	(168)	E	205	653	503	521	370	320	478	370	526	629	537	595	631	851	181	333	1047	1047	198	306	348	467	526	1513	143	527	629	878	901	
ø	Query	Match	96.5	76.8	76.8	35.9	35.6	35.6	35.2	34.9	34.5	33.8	33.8	33.8	33.5	33.5	33.1	33.1	32.7	32.7	32.7	32.7	32.4	32.4	32.4	32.4	32.4	32.4	32.0	32.0	32.0	31.7	31.7	
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P32868 reovirus (t	P35632 arabidopsis	P52045 escherichia	~	•			Q96rd7 homo sapien	_	070628 mus musculu		P34722 caenorhabdi
S_REOVJ	AP3_ARATH	G_ECOLI	2_ENTHI	ALSB_ECOLI	2_ENTHI	B_RABIT	PAN1_HUMAN	C_PSEAE	A MOUSE	1_ARATH	TPC1_CAREL
1 VSI	1 AP3	1 YGE	1 ACP	1 ALS	1 CPP	1 E2B	1 PAN	1 RMD	1 CN9	1 HT3	1 KPC
125	232	261	310	311	315	351	422	453	534	661	704
31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0	31.0
44	44	44	44	44	44	44	44	44	44	44	44
34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 Bc1-2 homology 3 (BH3) domain.
SIMILARITY: BELCHORS TO THE BCL-2 FAMILY.
CAUTION: Ref. 1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor signaling and the apoptotic pathways.
SUBDNIT: Rorms heterodimers with the anti-apoptotic proteins, Bcl-
x(1), Bcl-2 and Bcl-w. Also binds protein $100A10 (By similarity).
The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylation, locates to the cytoplasm.
TISSUE SPECITICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
PTM: Phosphorylated on Ser-75 in response to survival stimuli. Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-99 is the major site of ART/PKRB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimentation of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor
                                                                                                                                                                                                                                                                                                                                                  Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rationale for Bcl-xL/Bad peptide complex formation from structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PKA AND PKB) (BY
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000712; BG12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 603167; -. C:cytoplasm; NAS. GO: GO:0005737; C:cytoplasm; NAS. GO: GO:0005741; C:mitochondrial outer membrane; NAS. GO: GO:00005151; F:protein binding activity; NAS. GO: GO:0008632; P:apoptotic program; TAS. GO; GO:0008637; P:induction of apoptosis; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutagenesis, and biophysical studies.
Protein Sci. 9:2528-2534(2000).
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                                                                                                                                                                                                                                                                                                SINCLIONE BI NAM OF 103-12/;
MEDLINE=21073561; PubMed=11206074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF021792; AAB72092.1; -.
EMBL; AF031523; AAB88124.1; -.
EMBL; BC001901; AAH01901.1; -.
                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 103-127
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75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1G5J; 07-FEB-01
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ILSUGENCE FROM N.A.
IISSUGEBRAIN, and Thymus;
MEDLINE=95136361; PubMed=7834748;
Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
Yang a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
"Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "14-3-3 proteins and survival kinases cooperate to inactivate BAD by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98022383; PubMed-9381178;
Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.,
"Interleukin-3-induced phosphorylation of BAD through the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B., Greenberg M.E.;
                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BCl2-EB-2003 (Rel. 41) (BAD) (BCl-2 binding component
                                                                                                          Length 168;
                                                                                                                                                Indels
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PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
SIMILARITY).
A -> S (in dbSNP:3729933).
                                                       121
18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                      Score 137; DB-1;
Pred No. 8.2e-13;
0; (Mismatches 1)
                                    /FTIG=VAR_015380
                                                                                                                                                                                                                                                                                                                                                                                                                              (Bcl-xi/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                  204 AA.
                                                                                                                                                                                                      103 NIWAAQRY&RELRRMSDEFVDSFKKGL 129
                                                                                                                                                                         1 NLWAAQEYGRELRRMSDEFVDSFKKGL
                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH3 domain phosphorylation."; Mol. Cell 6:41-51(2000).
                                                                                                             96.5%;
96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 278:687-689(1997).
                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                         168 AA;
                                                                                                             Query Match
Best Local Similarity
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S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
Interference of BAD (Bcl.*ZL/Bel-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia: Eutheria: Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21109372; pubMed-11161472; Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.; "Functional characterization of two splice variants of rat BAD and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-98194755; Pubmed-9535132; D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator
                                                                                                                                                                                                                PKB).
PKB).
PKB).
                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               035147; 070256; 09JHX1;
16-0CT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                              Score 109; DB 1; Length 204;
Pred. No. 1.2e-08;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
Contains 1 Bcl-2 homology 3 (BH3) domain. BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                              PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND
                                                                                                                                                                                                                                                                                         6C2BA910205053F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                     205 AA.
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BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                         1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                          HSSP, 092934; 1G5J.
MGD; MGT:1096330; Bad.
InterPro; 1PR000712; Bc12_BR.
PROSITE; PG01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. Lett. 243:137-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98034386; PubMed=9369453;
                                                                                                                                                                                                                                                                                        204 AA; 22080 MW;
                                                                                                                     EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                             76.8%;
87.5%;
                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 87.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                             112
136
155
112
1136
155
                                                                                                                                 PIR; A55671; A55671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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between the Swiss Institute of Bioinformatics and the EMBL outstation—
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
their interaction with Bcl-w in sympathetic neurons.";

Mol. Cell. Neurosci. 17:97-106(2001).

-: FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-: Subunit; Porms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein SlOAAIO. The Ser-113/Ser-137 phosphorylated form binds 14-3-3 proteins.

-: SubcEllUlaria IcORFINON: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bowaln form.

DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX thair pro-apoptoric activity and for their interaction with anti-apoptoric members of the Bcl-2 family.

PTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKFNER phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=035147-2; Sequence=VSP_000534; risous specification: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial colls of the choroid plexus, Isoform alpha is the more abundant form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S->A: NO HETERODIMERIZATION WITH 14-3-3 PROTEINS. NO EFFECT ON HETERODIMERTZATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTIG=VSP_000534.
S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major site of protein kinase A (CAPK) phosphorylation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOR WITH PROTEIN P11.
ERRGRK (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGR -> ERRGRK (IN REF. 1).
7AFA71DAE9CF4A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity). SIMILARITY: Contains 1 Bcl-2 homology \overline{\mathbf{3}} (BH3) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Alpha;
IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WITH BCL2 1
SDAGGR -> 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF003523, AAC53374.1; -.
EMBL, AF031227, AAC15100.1; -.
EMBL, AF279910, AAF91427.1; -.
EMBL, AF279911, AAF91428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SE
22228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000712; Bcl2_BH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.8%;
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205 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
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       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Behrens B., Noyer-Weidner M., Pawlek B., Lauster R., Balganesh T.S.,
Trautner T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trautner T.A.;
Submitted (SEP-1987) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS ENZYME METHYLATES CYTOSINE WITHIN THE SEQUENCES
GGCC AND GAGGTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = adenosyl-L-homocysteine + DNA 5-methylcytosine.
-!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Organization of multispecific DNA methyltransferases encoded by temperate Bacillus subtilis phages.";
EMBO J. 6:1137-1142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1985 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annocation update)
Modification methylase Rholls1 (EC 2.1.1.73) (Cytosine-specific methyltzansferase Rholls1) (Bs Plls) (M.Rholls1).
                                                                                                                                                MIM; 602290; -.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003713; F:transcription co-activator activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 1; Length 653; 
Pred. No. 11; 
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          RING-TYPE.
B BOX-TYPE.
F -> I (IN REF. 1).
D83B1595CA8378FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87246516; PubMed=3109889;
                                                                                                                                                                                                   Interpro; IPR001258; NHL.
InterPro; IPR001358; NHL.
InterPro; IPR001341; Znf_Bbox.
Interpro; IPR001841; Znf_ring.
Pfam; PF00436; NHL; 5.
Pfam; PF00643; Zf-B_box; 1.
SMART; SM00136; BBOX; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS001818; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QEYGRELRRMSDEFVDSFK 24
                                                                             EMBL; AL133284; CAB92723.1; -. EMBL; BC003154; AAH03154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 F
71988 MW;
                                                            EMBL; U18543; AAA86474.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.9%;
                                                                                                                               HGNC:16380; TRIM32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        65
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage rho-11s.
                                                                                                                HSSP; P29590; 1BOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
REVISION TO 476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTBR_BPRH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZN_FING
ZN_FING
                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
MTBR_BPRH1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the Furopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A RIGHTON DEATON FOR THE STATE AND DEATOR TO STAND MADELINE 2.2.8. FEIRGOLD E.F., GTOUSE L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A litechal S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mans S.I., Wang J., Hsieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soarses M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley R.C., Hale S., Carninci P., Prange C.,

Robers S.A., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzoy D.M., Sodergren E.J., Lu X., Gibbs R.N.,

Raha S.S., Worley K.C., Hale S., Scherchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C.,

Rochiguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rothiguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length

R. Groen S. W. May PROFENS IN IN VIVO. BINDS SPECIFICALLY TO

THE AUTVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INFERACT WITH THE

C. THE AUTVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INFERACT WITH THE

C. SHORTH BLAY THE PROPENS IN VIVO.
                      ó
                                                                                                                                                                                               013049; Q9NQP8; Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-containing protein HT2A (72 kDa Tat-interacting protein) (Tripartite TRIM32 OR HT2A.
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.;
"Identification of a novel human zinc finger protein that
specifically interacts with the activation domain of lentiviral Tat
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY,
                      ;
0
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 B box-type zinc finger.
                    ŝ
     Pred. No. 1.2e-08;
                                                                                                                                                                                    653 AA.
                    Mismatches
                                                                                            141 NLWAAQRYGRELRRMSDEFEGSFK 164
                                                          1 NLWAAQEYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-95297135; PubMed=7778269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear
                      ;
0
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 209:347-357(1995),
                      21; Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTESTINE AND COLON.
                                                                                                                                                                                                                                                                                                                           (Human)
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sehra H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins
                    Matches
                                                                                          g
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Gaps

0;

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Gaps

1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPTRUVATE (PEP)
AND D-PERYTHROSE-4-PHOSPHATE (B4P) GIVING RISE TO 3-DEOXY-D-ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-92225349; PubMed=1348717;
Klenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
Klenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
"Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doignon F., Biteau N., Aigle M., Crouzet M.; "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUTPase in a yaast.".
                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 24, Last sequence update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-barabino-heptulosonate 7-phosphate synthase).
ARO4 OR FBR249C OR FBR1701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate phosphate + phosphate = phosphoenolpyruvate + D-erythrose phosphate + H(2)0.

BN2YME REGULATION: INHIBITED BY TYROSINE.
                                                           Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               first step.
-!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
     ATP (BY SIMILARITY).
1783A3320B106341 CRC64;
                                                                                            8,
                                                         DB 1;
                                                       Score 50.5; DB
Pred. No. 9.9;
9; Mismatches
                                                                                                                                                                                                                                                       370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                              481 NTWKDKEEYDKTAKRLAQRFIENFQK 506
                                                                                                                             1 NLWA-AQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94078675; PubMed=8256522;
     234 AI
58771 MW;
                                                                                                                                                                                                                                                                                      01-OCT-1993 (Rel. 27, Created)
                                                         35.6%;
                                                                         ilarity 30.8%;
Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               durpase in a yeast.";
Yeast 9:1131-1137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 113:67-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO 205-207.
     227 2
521 AA;
                                                                      Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuenzler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY:
                                                                                                                                                                                                                                                       AROG_YEAST
     NP_BIND
SEQUENCE
                                                           Query Match
                                                                                                                                                                                                                                      AROG_YEAST
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          + +
                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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     Noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PD004723; PEPCK ATP; 1.
TIGRPAMS; TIGR00224; pckA; 1.
PROSITE; PS00532; PEPCK_ATP; 1.
Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP]
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang J.,
., Ling L.,
                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                         503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [Rp] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MB4 / JCM 11007,
MEDLINE=11992816; PubMed=11997336;
BAO Q. Tian Y. Li W., Xu Z., Xuan Z., Hu S., Dong W., Yan Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y.,;
Tan H., Chen R., Mang J., Yu J., Yang H.;
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                       DB 1; Length
                                                                                                                                                                                                                                                                                    AAAFB8FE01B8129E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                               PRINUS; rrouse, TigRoOf5; don; 1. PROSITE; PS00094; C5_MTASE 1; 1. PROSITE; PS00095; C5_MTASE_2; 1. Transferase; Methyltransferase; Restriction system. Transferase; PS SIMILARIA BY SIMILARIA
                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521 AA.
                                                                                                                                                                                                                                                                                                                                            9.5
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                       35.6%; Score 50.5; 50.0%; Pred. No. 9.
                  entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                     HSSP, P05102; 6MHT.
REBASE; 2835; M.RhollsI.
InterPro; IPR001525; C5_DNA_meth.
Pfam; PF00145; DNA_meth/lase; 1.
PRINTS; PR00105; C5METTRFRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                |:||: || || ::|||
207 WSAQDIVGRRLREILEEYVD 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                              3 WAAQE-YGRELRRMSDEFVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE013131; AAM24977.1; -.
                                                                                                                                                                                                                                                                                  57129 MW;
                                                                      EMBL; X05242; CAA28869.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01293; PEPCK_ATP;
                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                    503 AA;
                                                                                          CTBPRH
                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCKA OR TTE1783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPCK_THETN
                                                                                          PIR; A28137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + CO(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                    ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPCK_THETN
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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7-4

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EMBL; AE003721; AAF55514.1; ALT_SEQ.
EMBL; AY058248; AAL13477.1; -.
FlyBase; Fep0038585; CG7993.
Infarpro; IRROD109; Brix.
Pfam; PF04427; Brix; 1.
Hypothetical protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 WAQTE---ELRRLRNLFIDTFQR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 WAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                   STRAIN-Berkeley;
MEDLINE-22426066; PubMed-12537569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 2322 / CBS 819;
MEDLINE-95339407; PubMed-7614556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=27300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HXK DEBOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rose M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HXK_DEBOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
        QΫ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RADDLINGE_LUL90UD; PUDMORE_LUTS1;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.E.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Elazej R.G., Champe M., Pfeiffer B.D.,

RA Brank M.L., Doyle C., Baxerer B.G., Helt G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Bulck H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bulke C., Davenport U.B., Davies P.,

RA Burtis K.C., Busam D.A., Bulke C., Davenport U.B., Davies P.,

RA Burtis K.C., Busam D.A., Bulke C., Davenport U.B., Davies P.,

RA Gerry J.M., Cawley S., Dahlke C., Davenport U.B., Davies P.,

RA Burtis K.C., Busam D.A., Bulke C., Davenport U.B., Davies P.,

RA Goden K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Glodek A., Gony F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston R.A., Howland T.J., Wei M.-H., Ibeyam C.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Liu X., Mattei B., McIntosh T.C., McGed M.P., Pachelb J.M.,

RA Mount S.M., Moy W., Murphy B., Murphy L., Mursy D., Duri V., Reese M.G.,

RA Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling R.C., Turner R., Venter E., Wang A.H., Wang X.,

RAIrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                           0
EMBL; X61107; CAA43419.1; -.

EMBL; L20296; AAA55607.1; -.

EMBL; Z36118; CAA65512.1; -.

EMBL; S38185; S38185.

HSSP; P00886; 1QR7.

SGD; S0000453; ARO4.

GG; GG:0003499; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA. InterPro; IPR006219; AroFGH.

InterPro; IPR006219; AroFGH.
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Busaryota, Metazoa, Arthropoda; Hespoda, Insecta, Pterygota, Neoptera; Endopterygota, Diptera, Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                InterPro; IPR006218; DAHP1/KDSA.

Pfam; PF00793; DAHP_synth_1; 1.

ProDom; PD005060; AroFGH; 1.

TIGRPAMS; TIGR00034; aroFGH; 1.

Aromatic amino acid blosynthesis; Lyase; Multigene family.

SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                            DB 1; Length 370;
                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Brix domain containing protein 1 homolog.
                                                                                                                                                                                                                                            Score 50; DB 1
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 320 AA.
                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                              097053; 095084;
16-0CT-2001 (Rel. 40, Created)
15-SEP-2003 (Rel. 42, Last sequ
15-SEP-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                         1 NLWAAQEYGRELRRMSDE 18
                                                                                                                                                                                                                                                                                                                             35.2%;
55.6%;
                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                      BXD1_DROME
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG7993
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
BXD1_DROME
                                                                                                                                                                                                                                                                           Matches
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Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L., Zhong X., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular and biochemical characterization of the hexokinase from the starch-utilizing yeast Schwanniomyces occidentalis.";
Curr. Genet. 27:330-338(1995).
-!- CATALYIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-!- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
-!- SUBDINIT: HOMOGIMET (By similarity).
-!- SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.9%; Score 49.5; DB 1; Length 320; Best Local Similarity 43.5%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 188 I -> T (IN REF. 1).
320 AA; 36509 MW; EE98936DD68B3703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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01-0CT-1996 (Rel. 34, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
HEXOKinase (EC 2.7.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
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VP5_BTV2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the ARO4 gene encoding a second DAHP synthase.",
Curr. Genet. 29:441-445(1996).
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-PERYTHROSE 4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pereira S.A., Livi G.P.;
"Aromatic amino-acid biosynthesis in Candida albicans: identification
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAEP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-phosphate + H(2)0.
                                                                                                                                                                                                                                                         Transferase; Kinase; Glycolysis; Allosteric enzyme; ATP-binding. BINDING 111 111 ATP (BY SIMILARIY).
151 177 GLUCOSE-BINDING (POTENTIAL).
SEQUENCE 478 AA; 53066 MW; 080D5F9134479ABA CRCG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                 34.5%; Score 49; DB 1; Length 478; 42.1%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sousa S., Pereira S.A., Livi G.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 AA.
                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                  InterPro; IPR001312; Hexokinase.
Pfam; PF03727; hexokinase2; 1.
Pfam; PF00349; hexokinase; 1.
PRINTS; PR00475; HEXOKINASE.
PRODOM; PD001109; HEXOKINASE; 1.
PROSITE; PS00378; HEXOKINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A. MEDLINE-96207468; PubMed-8625423;
                                                                                                                                                                                                                                                                                                                                                                                                                  38 GETLRKITDHFISELEKGL 56
                                                                                                                                                                                                                                                                                                                                                                                       9 GRELRRASDEFVDSFKKGL 27
                                                                                                                            EMBL; S78714; AAB34892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 11651 / B792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                       PIR; S57203; S57203.
HSSP; Q26609; 1BDG.
                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AROG_CANAL
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Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-9020938; PubMed=2157314;

Hirasawa T., Roy P.;

"The complete nucleotide sequence of VP5 of a strain of bluetongue virus of serotype 1 isolated in the USA reveals its close relationship with a virus of serotype 1 isolated in Australia.";

Virus Res. 15:107-112(1990).

-: FUNCTION: THE VP5 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP2)

WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.

-: SIMILARITY: BELONGS TO THE REOVINGESS VP5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Prodom; PD005060; AroFGH; 1.
TIGRPAMS; TIGR00034, aroFGH; 1.
Aromatic amno acid hiosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 40291 MW; 11E5E324C8D7B6DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 1; Length 370;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.8%; Score 48; DB 1; Length 526; 41.7%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bluetongue virus (serotype 2 / isolate USA). Viruses; dsRNA viruses; Reoviridae; Orbivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Outer capsid protein VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                      HSSP; P00886; 1QR7.
InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHPI/KDSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR: A43486; PSXRBU.
InterPro; IPR000145; orbi_vP5.
Pfam; PF00901; Orbi_VP5; 1.
Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 ALEYGKRLKKLADELKD 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%;
47.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AQEYGRELRRMSDEFVD
                                                                                                                                                                                 EMBL; U53216; AAB48240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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Best Local Similarity
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Best Local Similarity
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EMBL; X63291; CAA44925.1; -. HSSP; P22259; IAQ2.
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                               STANDARD;
                            301
629
125
128
146
300
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Best Local Similarity
Matches 10; Conserva
                                                                                                                            629 AA;
                                                                                                                                                                     Similarity
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RNA-binding;
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                                                                                                                                                        Query Match
Best Local S
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                                                                                                                BINDING
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                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Is required not only for elongation of protein synthesis but also for the initiation of all mRNA translation through initiator tRNA(fMet) aminoacylation (By similarity).
-!- CAPALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP + diphosphate + L-methionyl-tRNA(Met).
-!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SERALNeWEBB / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

Haft D.H., Hickey E.K., Malek J.A., Linher K.D., Garrett M.M.,

Stoopald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

"Exidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                      15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
                                                                                                                            Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                         Guipaud O., Marguet E., Noll K.M., de la Tour C.B., Forterre P., "Both DNA gyrase are present in the Myperthermophilic bacterium Thermotoga maritima."; Proc. Natl. Acad. Sci. U.S.A. 94:10606-10611(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetG subfamily 2A.
-!- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0398; metG; 1.
TIGRRAMS; TIGRO0399; metG_C_term; 1.
PROSITE; PSO0178; AA_TRNA_LIGASE_I; FALSE_NEG.
PROSITE; PS50886; TRED; 1.
             629 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00133; tRNA-synt_1; 1.
Pfam; PF01589; tRNA-bind; 1.
PRER; PIRSF001528; MetRS_dimerising;
PRINTS; PR01041; TRNASYNTHMET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; TM1085, -
HAMAP: MF-01228; fused; 1.
InterPro; IPR004495; MetG_Cterm.
InterPro; IPR001300; tRNA-synt_1a.
InterPro; IPR0012304; tRNA-synt_I.
InterPro; IPR0012304; tRNA-synt_I.
InterPro; IPR002304; tRNA-synt_I.
              PRT;
                                                                                                                                                                                                STRAIN=MSB8 / DSM 3109;
MEDLINE=98021416; PubMed=9380682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE001768; AAD36162.1; -.
PIR, E72297; E72297.
HSSP; P23395; 1A8H.
                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U76417; AAB87143.1; -.
                                                                                                               METG OR METS OR TM1085.
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=2336;
             SYM_THEMA
                                                                                                   (Metrs)
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MEDLINE-20179905; Pubmed=1720862;
Oesteraas M., Finan T.M. Stanley J.;
Oesteraas M., Finan T.M. Stanley J.;
"Site-directed mutagenesis and DNA sequence of pckA of Rhizobium
NGR234, encoding phosphoenolpyruvate carboxykinase: gluconeogenesis
and host-dependent symbiotic phenotype.";
Mol. Gen. Genet. 230:257-269(1911).
-i- CATALYTIC ACTIVITY: AIP + oxaloacetate = ADP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: Rate-limiting gluconeogenic enzyme.
-i- SUBCELDLAR LOCATION: Cytoplasmic (By similarity).
-i- SIMLIARITY: Belongs to the phosphoenolpyruvate carboxykinase [ATP] family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
tRNA-binding, Metal-binding, Zinc, Complete proteome.
10 20 "HIGH" REGION.
197 301 "KMSKS" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [RP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase)
                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 1; Length 629; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                        ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).

W, BOE0759F7C78ACEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobia
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rP (BY SIMILARITY).
B2CED7FA54326B1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; WF_00453; -; 1.

InterPro; IRR001272; PEPCK_ATP.

Pfam; PF01293; PEPCK_ATP; 1.

PROD04723; PEPCK_ATP; 1.

IGRPAMS; TIGR00224; pckA; 1.

PROSITE; PS00532; PEPCK_ATP; 1.

PROSITE; PS00532; PEPCK_ATP; 1.

RUCONDOGOROSIS; Lyase; Decarboxylase; ATP-binding.

NP_BIN B ARP (BY SIMILARITY).

SEQUENCE 537 AA; 58370 MW; B2CED7PA54326BIE CRC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.5%; Score 47.5; D
41.7%; Pred. No. 28;
iive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                 TRNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LWAAQEYGRELRRMSDEFVDSFKK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||: |:: : || : ||:
LQAAQQAGKDPQEFCDELAEKFKR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                         73004 MW;
                                                                                                                                                                                                                                                                                                                                                         33.8%; 37.5%; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium sp. (strain NGR234)
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Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PIR; G70188; G70188.
HSSP; P00579; 1SIG.
TIGR; BB0712; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                 BACTERIA
                                                                            burgdorferi.
                                                                                                                            STRAIN=297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions in its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-PROCC 35210 / B31;
MEDLINE-98065943; bubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                   MEDINE-98300335; PubMed=9636706;
Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
"Genome structure of mycobacteriophage D29: implications for phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Spirochaetes; Spirochaetales; Spirochaetaceae, Borrelia
NCBL_TaxID=139;
                                                                                                                                                                                    no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, TPR005021; Phage_termin.
Pfam, PF03354; Phage_terminase; 1.
SEQUENCE 595 AA; 66397 MW; AFD123ED5371E263 CRC64;
                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE PHAGE TERMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thesis (1994), National Taiwan University, Taiwan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                     595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA polymerase sigma factor rpoD (Sigma-70) RPOD OR BB0712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.5%; Score 47.5; 45.5%; Pred. No. 31
            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::| |:|| |: | |||| |: 435 DIWDPQKYGGEVPR---EFVDA 453
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NLWAAQEYGRELRRMSDEFVDS 22
3 WAA-QEYGRELRRMSDEFVDSFKK
                                                                                                                                                                                                                                                                                    J. Mol. Biol. 279:143-164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF022214; AAC18453.1; -. PIR; B72801; B72801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 89-631 FROM N.A. STRAIN=ATCC 35210 / B31; Pan M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 45.5
nes 10; Conservative
                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                       Mycobacteriophage D29.
Viruses; dsDNA viruses,
NCBI_TaxID=28369;
                                                                                                                                                Gene 13 protein (GP13).
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                   VG13_BPMD2
O64206;
                                                                                                                                                                                                                                                                           evolution."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                         VG13_BPMD2
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                                                           RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             Pan M., Yeh J., Tsai C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENY OF THE WAR POLYMERABE TO SPECIFIC INTITIATION SITES AND
THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000943; Sigma_70.
Pfam; PF03979; sigma70_rl_1; 1.
Pfam; PF00140; sigma70_rl_2; 1.
Pfam; PF04542; sigma70_rr2; 1.
Pfam; PF04545; sigma70_rr2; 1.
Pfam; PF04545; sigma70_rr3; 1.
PROSITE; PS00715; SIGMA70_r; 1.
PROSITE; PS00716; SIGMA70_r; 1.
Transcription_regulation; Sigma factor; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
       Hanson M.
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M. van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Warthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.; Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 POLYMERASE CORE BINDING (POTENTIAL).
608 H-T-H MOTIF (BY SIMILARITY).
73642 MW, BD565AB7D8F44796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 23, 2003, 09:47:46
Job time: 26 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 YQEELRIFSDDYIDSANK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Complete proteome.
DOMAIN 419 432 PO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U17591; AAC44104.1; -.
EMBL; AE001171; AAC67061.1; -
EMBL; U68006; AAC45100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                SEQUENCE OF 165-614 FROM N.A.
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Scoring table:

Searched:

Database

Perfect score:

Sequence:

protein

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on:

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299bu0 potato mop-

08vjs3 mycobacteri

010843 mycobacteri

0910843 mycobacteri

094062 pseudomonas

09fq05 atrichum an

08ppy8 xanthomonas

09fu63 arrichum an

09fu64 aryaz aativ

09fu64 oryaz aativ

09fu64 oryaz aativ

09fu64 oryaz aativ

09fu64 oryaz aativ

09fu65 oryaz aativ

09fu66 bluetongue
                                                                                                                                                                               QERAPS YETAINED PE
QERAPS YETAINED PE
QOQUUS STABPINGOCO
QOWAZI Drassica ol
QOSTÓ arabidopsis
QOSTI arabidopsis
QOSTI arabidopsis
QOSTI prassica ca
                               Q9hklO thermoplasm
Q97bl5 thermoplasm
Q8r937 thermoanaer
                Q8tme7 methanosarc
                                                                                                                                                                  arabidopsis
                                                                                                                                                                         archaeoglob
                                                        clostridium
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                  Q8gui8
029007
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                                                        Q97h37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           zebrafish.";

Cell Death Differ. 7:509-510(2000).

EMBL, AR731017, AAF66962.2; -.

HSSP, Q9294, 1G5J.

ZEIN; ZDS-GENE-000616-1; bad.

SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.2%; Score 84; DB 13;
Best Local Similarity 62.5%; Pred. No. 0.00023;
Matches 15; Conservative 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 AA.
                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LWAAQEYGRELRRMSDEFVDSFKK 25
                                                        Q97H37
Q9QBU0
                                                                                        0941D5
09HY62
09FQ05
08PPY8
0941D4
09FU53
0941E4
08BAD7
                                                                                                                                                                         029007
Q8ZAP2
                                                                                                                                                                                         099003
08W4Z1
09SXJ6
094JY6
082421
09ST19
                                                                                                                                                                                                                                                                                                                    Created)
                                       Q97B15
Q8R937
                                                                        Q8VJS3
Q10843
Q8PYK0
Q9RUK9
Q8TME7
                                                                                                                                                                  QBGUIB
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
01-OCT-2000 (TrEMBLE), 15,
01-DEC-2001 (TrEMBLE), 19,
01-OCT-2002 (TrEMBLE), 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8H4M3
Q8H4M3;
                                                                                                                                                                                                                                                                                                   Q919N2
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                                                                                                                                                                                                                                                                                  RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
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ID Q8
AC Q8
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Q818y1 thermoaneer
Q81mf2 oryza sativ
O64692 arabiobsis
Q81mg2 pseudomonas
Q91mg3 pseudomonas
Q81mg55 homo sapien
Q81mg6 shewanella
Q81mg6 shewanella
Q91mg7 shewanella
Q94mg6 drosophila
Q95mg4 drosophila
Q95mg4 drosophila
Q95mg4 drosophila
Q95mg4 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9i9n2 brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    September 23, 2003, 09:43:16; Search time 96 Seconds (without alignments) 72.577 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                 830525
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                142
1 NLWAAQEYGRELRRMSDEFVDSFKKGL 27
                                                                                                                                                830525 segs, 258052604 residues
                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0919N2
08R8Y1
08R8Y1
08LMF2
06LMF2
09HZQ3
09HZQ3
08HSQ3
08F5R1
08F5R1
09F5R1
09W5B6
09W5B6
09W5B6
                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                         sp_unclassified:*
                                                                                                                                                                                                                                                                                                                       sp_plant:*
sp_rodent:*
sp_voints:*
sp_virus:*
sp_vertebrate:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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sp_bacteria:*
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                                                                                        US-09-544-664B-2
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                                                                                                                                                                                                                                                                                          sp_mammal:*
sp_mhc:*
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                                                                                                                                                                                                                                                                          sp_human:*
                                                                                                                                                                                                                                         SPTREMBL 23:*
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606
889
335
722
1248
173
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214
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Match Length
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Score

Result 8

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Enssicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                      STRAIN=CV. Nippondare; McComble M., Spiegel L., Preston R., Ferraro K., McComble W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K., Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J., Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.; Genome C. O'Shaughnessy A., Palmer L., Dedhia N.; Submitsed G. O'Jaszbob, from chromosome 10, complete sequence."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae, Oryzae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                      36.6%; Score 52; DB 10; Length 889; 40.0%; Pred. No. 79; 1. of Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.9%; Score 51; DB 10; Length 335; 37.5%; Pred. No. 37;
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889 AA; 101583 MW; C47D8715883D6376 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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EMBL, AC0404077. AAM14998.1; -
InterPro; IPR005123; 20G-PeII_oxy.
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136 AVEEYIKEMKRMSSKFLEMVEEEL 159
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T31E10.11 OR GA20X3.
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Matches 10; Conservi
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Matches 9; Conserv
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                                                                         NCBI_TaxID=39947;
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SEQUENCE 88
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STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
BaO Q. Tlan Y., Li W. Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yang H.;
Tan H., Chen R., Wang J., Yu J., Yang H.;
Ba Complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002)
EMBL; AE013137; AAM25042.1;
Hypothetical protein; Complete proteome.
                                                                                     Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae: Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
Noryaa sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OJ1116_C08.";
Submitted (AGG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; APPO4002: BACC0651.1; -
ERDDUSENCE 606 AA; 68758 MW; D453BODEF5AE2D94 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Length 606;
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein TTE1854.
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Last annotation update)
                01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
031116_C08.8 protein.
031116_C08.8.
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Pred. No. 26;
8; Mismatches 7;
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40.0%;
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Best Local Similarity 40.00,
"hea 10; Conservative
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Matches 9; Conservative
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                                                                                                                                                             NCBI_TaxID=39947;
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28TVX8; Q8TVX8

RESULT 6

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Tasgue-Brain;
Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Iris R., Otsuki T., Sato H., Ota T., Wakamatu A.,
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO95662; BACO4601.1;
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A Arlat M., Billault A., Brottier P., Camus J.C., Catcolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
A Waissenbach J., Boucher C.A.;
T. "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
R EMBL; ALG46067; CAD15739.1; -.
R InterPro; IPR003439; ARA_ATPase.
R InterPro; IPR003439; ARA_ATPase.
R Pfam; PF00005; ABC_tran; 1.
Gaps
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
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5; Indels
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SEQUENCE 173 AA; 21285 MW; 0EBFF3BFD96FE775 CRC64;
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01-MAR-2002 (TrEMBIREL 20, Last sequence update)
01-MAR-2003 (TrEMBIREL 23, Last annotation update)
Probable ATP-binding ABC transporter protein.
                                                                                                                                                                                                                                                01-OCT-2002 (TIEMBLED. 22, Created)
01-OCT-2002 (TIEMBLED. 22, Last sequence update)
01-MAR-2003 (TIEMBLED. 23, Last annotation update)
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4; Mismatches
5; Mismatches
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MEDLINE=21681879; PubMed=11823852;
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                                             2 LWAAQEYG--RELRRMSDEFVDS
                                                                                                                                                                                                                                                                                                                      Hypothetical protein FLJ38343.
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Local Similarity 47.6%;
les 10; Conservative
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11; Conservative
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Q8XXS6
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Q8N955
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STREIN-ATCC 15692 / PAO1;
STREIN-ATCC 15692 / PAO1;
SX BEDINE-2043737; PubMed-10984043;
STREIN-ATCC 15692 / PAO1;
SX BEDINE-2043737; PubMed-10984043;
SX HOLLINE-2043737; PubMed-10984043;
SX Garber C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
SX Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Tuan Y.,
SX Garber R.L., Goulter S.W., Folger K.R., Kas A., Larbig K., Lim R.W.,
SMITH K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
REL; ABOU4720; A&G0663321; -.
InterPro; IPRO03672; CobN/Mg_chltase.
InterPro; IPRO0408; Reg_chr_condens.
PROSITE; PS00626; RCGL_2; 1.
                                                                                                                                                                              MK1260.
Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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                                                                                                                                                                                                                                                                                                                                                                                 Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Matale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.; "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and mnonphyly of archaeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.9%; Score 51; DB 17; Length 722; Best Local Similarity 42.9%; Pred. No. 8%; Matches 9; Conservative 7; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722 AA; 81933 MW; 7FA609E9868A997E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBIrel. 16, Last sequence update) 01-MAR-2003 (TrEMBIrel. 23, Last annotation update) Cobalamin biosynthetic protein CobN.
                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1248 AA.
                                             722 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                          Created)
                                                                                                                                                        Predicted ATPase of the AAA+ class.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635 AREHGKELRRKEEEYRNRVRK 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AQEYGRELRRMSDEFVDSFKK 25
                                                                                 01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 1248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                        NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COBN OR PA2944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=287;
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RESULT 7

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Louis C.;
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                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 5; Length 371; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Benos P.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                           39874 MW; D59DE879EA9BFCB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          759BA109E3C0AE36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                      .
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 16;
Pred. No. 56;
5; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL109630; CAB65878.1; -. FlyBase; FBgn0040337; EG:BACR7A4.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                             35.2%; Score 45.0%; Pred.
                                                                                                                                                                                                                           4 AAQEYGRELRRMSDEFVDSF 23
                                                                                                                                                                                                                                                          ||:|| :|:::|| | 69 AAKEYALKLKKLHDELSDEF 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004506; TrmU.
Pfam; PF038054; tRNA_Me_trans; 1.
TIGRPAMS; TIGR00420; trmU; 1.
SEQUENCE 371 AA; 41315 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.2%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13, 01-OCT-2002 (TrEMBLrel, 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TIEMBLRE]. 23,
CG3021 protein (LD29918p).
EG:BACR7A4.8 OR CG3021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 28.6
nes 10; Conservative
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EG:BACR7A4.8 protein.
EG:BACR7A4.8 OR CG3021.
                                                              363 AA;
                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                               Complete proteome.
SEQUENCE 363 AA;
TIGR; SO1361; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9W5B6; 0960Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W5B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09W5B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NW KW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leptospira interrogans.
Bacteria: Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
NCBL_TaxID=70863;
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0
                                                                                                                                 Score 50; DB 16; Length 230;
Pred. No. 34;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=56601 / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
9hospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%; Score 50; DB 16; Length 330; 39.3%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL. AE011338; AAN48051; -.
Lyase; Complete protecome.
SEQUENCE 330 AA; 36561 MW; 88495C834E497C8 CRC64;
                                                                                    7C3FDA1E7A19A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) DTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 LWASNQKAKDLINWSPEYGGRDGFKRGL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LWAAQEYGRELRRMSDEF--VDSFKKGL 27
ProDom; PD000006; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015580; AAN54426.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                    230 AA; 25231 MW;
                                                                                                                                       35.2%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                    6 QEYGRELRRMSDEF 19
                                                                                                                                                                Local Similarity 71.4 nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                            SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                           Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFBB3 OR LA1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AROF OR SO136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                            KEC.
Q8F5R1
T Q8F5R1
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Matches
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Q8EH69
                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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DR NW SO

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikloo G.L.G.,

RA Dallew R.M., Basua A., Baxter E.G., Helt G., Nelson C.R., Mikloo G.L.G.,

RA Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basua D.A., Barnan B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B. Davles P.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gena P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywan C.,

Alalah M., Kalush F., Karpen G.H., Ke Z., Kenigon J.A., Ketchum K.A.,

RA Liu K., Matles B., McIntosh Y.C., McIeod M.P., Morberson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Randerk D.R., Nelson K.A., Nixon K., Nuxopk D.M., Nelson D.L.,

Randerk B., Kodir K., Bowley B., Murphy L., Murny D.M., Nelson D.L.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier E., Spradling A.C., Staplecon M., Strong R., Smith T.,

Spier E., Spradling A.C., Staplecon M., Strong R., Smith T.,

Rand S.M., Woose T., Worley K.C., Wu D., Yang S., Yao Q., A.,

RA Fordy C., Wassarman D.A., Weinstock G.M., Weissenbach M.,

Rander S.M., Weers E.W., Ribin G.M., Venter J.C.;

RA Fordy S.M., Meers E.W., Ribin G.M., Venter J.C.;

Rander S.M., Meers E.W., Ribin G.M., Venter J.C.;

Rander S.M., Meers E.M., Rong F.W., Ronger F., Stanger F., Stepher F., Stepher F., Stepher F., Stepher F., Stepher F., Steph Barzon J., Adding J. Baldwin D., Baradon R.C., Rogers Y., Baradon J., An H., Baldwin D., Barzon J., Beson K.C., Sogers Y., Barzon J., An H., Baldwin D., Barzon J., Beeson K.C., Eusam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Andron M., Dorsert V., Doug L.E., Doyle C., Dresnek D., Farfan D., Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck T., Hoskins R.A., Hostin D., Howland T.J., McInch T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., McInchoh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Racial J., Paragas V., Park S., Patel B., Pfeiffer B., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., R. Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Submitted (MAR-2000) to the EMBL/GenBank/DD5J databases. Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Barman B., Carlson T.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smurniak F., Whitfield E., Ashburner M., Gelbart W.W., Rubin G.W., Mungall C.J., Lewis S.E., "Annotation of prosophila melanogaster genome.", submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. Science 287:2185-2195(2000). SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. 

SEQUENCE FROM N.A.

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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2201) to the EMBL/GenBank/DDBJ databases.
EMBL, Ar058248; AAL13477.1;
Flybase; FBgn0038585; CG7993.
STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall.
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR093419; AAR4578.3;
EMBL; AR051773; AAK93197.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.5; DB 5; Length 320;
Pred. No. 58;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 5; Length 389; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                            FlyBase; FBgn0040337; EG:BACR7A4.8.
InterPro; IPR004506; TrmU.
FIGHEN, PP03054; TRNA_Lrans; 1.
TICRPAMS; TIGR0420; trmU; 1.
SEQUENCE 389 AA, 43350 MW; 20C9405FFCC9FAE2 CRC64;
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320 AA; 36509 MW; EE98936DD68B3703 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein CT1131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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9; Mismatches
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149 WAQTE---ELRRIRNLFIDTFQR 168
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43.5%;
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Best Local Similarity 28.6
Matches 10; Conservative
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01-DEC-2001
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Q8KDC3
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OC Chlorobia; Chlorobia; Chlorobiales; Chlorobiaceae;
OX NCBL TaxID=1097;
RN [1]
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RE SIGNALN-ILS / ATCC 49552 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RX MEDLINE N.J. Nelson N.C., Haift D.H., Yang F., Hokey B.K., Deboy R., Gwinn M.L., Nelson W.C., Farerson J.C., Taxen T.C., Taxen T.C., Craven M.B., Radune D., Nommathevan J.; Rhouri H., White O., Gruber T.M., Ketchum K.A., Vanathevan J.; Rhouri H., White O., Gruber T.M., Retchum K.A., Vanathevan J., Rouri H., Bryant D.A., Fraser C.M.;
RX Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RX Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RY Photosynthetic, anacrobic, green-sulfur bacterium ";
Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
BR TIGRF CT1131; -
DR TIGRO0372; TIGRO0372; 1.
RY MYDOThetical protein; Complete proteome.
SEQUENCE 214 AA; 24004 MW; 56D389219D60B6AD CRC64;
Rest Local Similarity 37.0%; Pred. No. 43; Indels 2; Gaps 1;
Matches 10; Conservative 8; Mismatches 7; Indels 2; Gaps 1;
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Search completed: September 23, 2003, 09:45:06 Job time : 101 secs

97 D

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model protein search, OM protein - September 15, 2003, 17:16:01; Search time 38.1857 Seconds (Without alignments) 112.231 Million cell updates/sec Run on:

US-09-544-664-3 145 1 NIWAAQRYGRELRRMSDEFEGSFKGLP/27) Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

SIDSI/gcgdata/geneseq/genesegp-embl/AA1981.DAT:\*
SIDSI/gcgdata/geneseq/genesegp-embl/AA1982.DAT:\*
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SIDSI/gcgdata/geneseq/genesegp-embl/AA1990.DAT:\*
A\_Geneseq\_19Jun03:\* .: /SIDS1/gcgdata/geneseq/genesegp-emb1/AA1980.DAT:\* :: /SIDS1/gcgdata/geneseq/genesegp-emb1/AA1981.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Bcl2 polypeptide B	Shorter murine BAD	bcl-x(L)/bcl-2 ass	Murine BCL-XL/BCL-	Mutant BCL-XL/BCL-	Mutant BCL-XL/BCL-	Mutant BCL-XL/BCL-	Murine BAD protein	Longer murine BAD
ďI	AAB37003	AAB70370	AAR95168	AAW61315	AAW61316	AAW61317	AAW61318	AAW58832	AAB70369
B	21	22	17	19	13	13	13	13	22
% Query Match Length DB ID	27	162	204	204	204	204	204	204	204
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	145	145	145	145	145	145	145	145	145
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WPI; 2000-679325/66

Murine BAD protein	2 polypeptide	2 polypeptide	Bcl2 polypeptide B	2 polypeptide	5 protein for	an Bcl-xL/Bcl-	lif	Human BAD mutant a	Bad	Amino acid sequenc	Human BAD protein	Human ovarian anti	Human Bad peptide	inter	it Bc]	Mutant Bcl2 compet		Human Bad peptide	bcl-x(L)/bcl-2 ass	Mutant Bc12 compet	Human Bad peptide	Mutant Bcl2 compet	Mutant Bc12 compe	Human Bad peptide	Human Bad peptide				77		773	~	:12 comp	Himan Bad nentide
ABR39082	200	700	AAB37056	AAB37055	247	577	AAB13512	336	328	99/	308	ABP41630	362	516	348	349	361	362	516	349	361	ABG78488	348	861	361	362	348	349	349	361	861	862	848	AAI178611
24	21	21	21	21	18	13	21	22	22	22	24	23	23	23	23	23	23	23	17	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
204	26	26	27	28	166	168	168	168	168	168	168	201	24	25	25	25	25	25	23	25	25	25	25	52	25	23	25	25	25	25	25	25	25	25
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K																																		

#### ALIGNMENTS

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic\_leukemia; neurodegenerative disorder; AIDS; 2 Z Bcl2 polypeptide BH3 domain peptide #3. Wang J, Zhang Z, Shan S, AA. AAB37003 standard; peptide; 27 (UYJE-) UNIV JEFFERSON THOMAS stroke; myocardial infarction 06-APR-2000; 2000WO-US09352 99US-0128202 (first entry) WO200059526-Al. 07-APR-1999; Homo sapiens 12-OCT-2000. 28-FEB-2001 Huang Z, AAB37003; RESULT 1 AAB37003 

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                                                                                                                The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group is attached to the C-terminus of the peptide where the functional group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain to group is constant of the peptide, where the side chain functional group is COOH or two double bonds, cyclobutyl cyclopentyl cyclohexyl containing one or two double bonds, cyclobutyl cyclopentyl cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB7001-B37061 sepresent examples of the peptide portried of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agouist Bad. The peptide conjugate is called the cell death agouist Bad. The peptide conjugate is called the cell death agouist Bad. The peptide conjugate is called blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a conjugate is useful for modular characterized by cancer cells that express Bcl-2. The cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, nor manil lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful gor treating dispraces belonged anonyment of the conjugate is also useful for treating dispraced by concerd and peptide conjugate is also useful for treating dispraces belonged anonyment of the constant of anonyment of the conjugate is also useful for treating dispraces belonged anonyment of the conjugate is also useful for treating dispraces belonged anonyment of the conjugate is also useful for treating dispraces belonged and the constant of the conjugate is also useful for treating dispraces the conjugate is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 145; DB 21;
100.0%; Pred. No. 2.6e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB70370 standard; protein; 162 AA.
                                                                                       Claim 18; Page 17; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000WO-US11864.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB70370:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The present invention describes an isolated or synthetic polypeptide

[1] Comprising a less than full length amino acid sequence of a mutant bel-XL/Bcl-1 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Serli8 of a human BAD, Serl55 of a murine BAD (longer murine BAD) or Serl13 of a murine BAD. Serli5 of a murine BAD (longer murine BAD) or Serli3 of a murine BAD (longer murine BAD) or Serli3 of a murine BAD (longer murine BAD) or Serli3 of a murine BAD (longer murine BAD) or Serli3 of a murine and interpretaints of a murine BAD (longer murine BAD) or Serli3 of a murine and interpretaints of a murine BAD (longer murine BAD) or Serli3 of a murine BAD (longer murine BAD) or Serli3 of a murine BAD (longer murine) or notivity that promote cell survival or apoptosis. Other uses include to a cultified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                           New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bcl-x(L)/bcl-2 associated death promoter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "BH1 conserved amino acids'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 145; DB 22; 100.0%; Pred. No. 1.9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111..130
/note= "PEST sequence"
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                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 148-149; 157pp; English.
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(APOP-) APOPTOSIS TECHNOLOGY INC.
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                                                                                                                            WPI; 2001-138734/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA;
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Best Local Si
Matches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                 Zhou X;
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09-MAY-1996.

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The present invention describes mutant bad bell-injured associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) tusion proteins of mutant BAD protein able to decrease cell viability; (2) cusion proteins of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or inflammation and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated mutants with BCL-2 or BCL-XL but instead binds to 14-3-3 family better substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                           present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant BCL-XL/BCL-2 associated cell death regulator #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 145; DB 19;
100.0%; Pred. No. 2.4e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW61316 standard; Protein; 204 AA.
                                                                                                                                                            Claim 1; Fig 10; 95pp; English.
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Best Local Similarity 100.
Matches 27; Conservative
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WPI; 1998-261422/23,
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                        N-PSDB; AAV27833
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Synthetic.
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AAW61316
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the murine bcl-x(L)/bcl-2 associated death bcl-x (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of Dcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), but is much less effective at accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                 Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers
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+'ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW61315 standard; Protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. AIDS, senescence or ischaemia
                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 1; 130pp; English
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                                          95WO-US14246.
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Matches 27; Conservative
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                                                                                                                                   (UNIW ) UNIV WASHINGTON.
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                                                                                                                                                                                                                                                       N-PSDB; AAT29479
                                                                                                                                                                                       Korsmeyer SJ;
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                                          31-OCT-1995;
                                                                                         31-OCT-1994;
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Seguence

Query Match

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RESULT 4 AAW61315 07-0CT-1998

AAW61315;

30-APR-1998

Mus sp.

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Gaps

0;

Length 204; Indels

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Matches
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                                                                                              The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (2) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease. Modified Ser are used to creen for enhancers and inhibitors of serime-phosphatase. Inhibitors are potentially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                             phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                       in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-
                        New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 145; DB 19; Length 204; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant BCL-XL/BCL-2 associated cell death regulator #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW61317 standard; Protein; 204 AA.
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                                                                          Claim 7; Page 59; 95pp; English.
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N-PSDB; AAV27835.
                                                                                                                                                                                                                                                                                                                                                                                                   204 AA;
N-PSDB; AAV27834.
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Synthetic.
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polymotheotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated as pepticis ser potentially useful in hibbitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, and inhibitors of serime-phosphatase. Inhibitors of cells is determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated on the specified Ser, forming a product that does not beterodimenties with BCL-2 or BCL-XL but instead binds to 14-3-3 family serime that the cytosol, thus promoting cell survival. The mutants with the substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 145; DB 19; 100.0%; Pred. No. 2.4e-14;
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                                                                                                                                                      Claim 7; Page 60; 95pp; English
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es 27; Conserva
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                                                                               viral infection
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                                                                                                                                                             death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infammation and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, adetermined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the Specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family ser substituted cannot bind 14-3-3.
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                                                                                                                                               The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
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New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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Pred. No. 2.4e-14;
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                                                                                                    Claim 7; Page 60-61; 95pp; English.
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Best Local Similarity 100.0
...a 27; Conservative
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This sequence represents a novel serine-phosphorylated protein, BAD (BC1-X1/Rol-2 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator. Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased/Accreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, senescence, neurodegenerative disease, ischemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infertion, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Messuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
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Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
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                                                                                                                                                                 Claim 3; Fig 8; 61pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200110888-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1999;
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Youle RJ,
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                               Local
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Region
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                             AAU00220
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                                                                                                                                                                                                                                                                                                   δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                  for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inframmation and autoimmune diseases. The present sequence represents a specifically claimed longer murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method (M1) for inducing apoptosis in
                                                To comprising a less than full length anno acid sequence of a mutent boll. Selection as a sociated cell death regulator polypeptide (BAD) or its fragment, which contrains amino acid substitutions at Seril8 of a human BAD. Seril5 of a murine BAD (shorter murine BAD) or Seril3 of a murine BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, nootropic, antiischaemic, vulnerary, cytostatic, antiviral, antianthritic, antiinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polypucleotides can be used for screening candidate compounds and drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                    The present invention describes an isolated or synthetic polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 145; DB 22; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR39082 standard; Protein; 204 AA.
Claim 4; Page 148; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine BAD protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2002; 2002WO-US24177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-248168/24.
N-PSDB; ABZ81201.
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                                                                                                                                                                                                                                                                                                                                                                                                             204 AA;
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                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ABR39082
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described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a 168 residue amino acids equence (see ABR30081), where the peptide comprises saril2, ser135, or ser155, or their combinations. BAD has virucide activity. M1 is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human M2 is useful for treating a patient infected with HSV. The present sequence represents murine BAD, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents the amino acid sequence of Bad-DTTR apoptosis-modifying fusion protein comprising Bad gene sequence fused via a short linker to diphtheria toxin translocation domain (DTTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 145; DB 24; 100.0%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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/note= "10x histidine tag"
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Chimeric - Corynebacterium diptheriae.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NIWAAQRYGRELRRMSDEFEGSFKGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU00220 standard; Protein; 567 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu X, Collier RJ;
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27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            204 AA;
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target cell. The apoptosis-modifying fusion protein comprises at least

two domains: the DTR domain, which targets the fusion protein to the

crayet cell and the Bel-Mi domain, which modifies an apoptotic response

of the target cell. The fusion protein is useful for modifying

(inhibiting or enhancing) apoptosis in a target cell, such as neuron,

tymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or

hyper-proliferative cell or an adipocyte. It is also useful for reducing

apoptosis in a subject after transient ischaemic neuronal injury,

cspecially spinal cord injury. The fusion protein may be used to treat

various diseases and injury conditions through inhibition or enhancement

of apoptotic cellular response, including neurodegenerative discorders

cuch as Alzheimer's disease, Huntington's disease, spinal muscular

atrophy, stroke episodes and unrequlated cell growth as in tumours and

various cancers. The apoptosis-modifying fusion protein can be delivered

effectively throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 145; DB 22; Length 567; 100.0%; Pred. No. 7.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bcl2 polypeptide BH3 domain peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huang Z, Wang J, Zhang Z, Shan S,
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                                                                                                                                                                                                                                                                                                                                                         567 AA;
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or CONHEZ; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl The perided with a 1-5C straight or branched chain alkyl group, or benzyl The peptided ABB7001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bc1-2 superfamily pulpeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bc1-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that cancer characterized by cancer cells that consmall lung, renal or thyroid cancers, colorectal, gastric, nor small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for treating disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bol-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                               increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                95.2%; Score 138; 100.0%; Pred. No. 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            26 AA;
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when the R.Y group is attached to the Cterminus of the peptide, or a side chain of the peptide, where the side chain functional group is constanting one or cowniz, and R = 2.18c alkyl or alkoxy, 2.14c alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohaxyl optionally monsubstituted with a 1.5c straight or branched chain alkyl group, phenyl optionally monsubstituted with a 1.5c straight or branched chain alkyl group, or benzyl. The peptides Aba37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl.2). "mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl.2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that cancer characterized by cancer cells that cancer characterized by cancer calls that cancer includes prostate, colorectal, gastric, on-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic laukemia. The peptide conjugate is also useful for treating disorders characterized by immunodefliciency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma, melanoma; lymphocytic leukemia; neurodegenerative disorder; AlDS; stroke; myocardial infarction.
functional group of the side chain is NH2 or OH; or X = 0 or NH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.2%; Score 138; DB 21;
100.0%; Pred. No. 3e-14;
iive 0; Mismatches 0;
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Claim 18; Page 19; 74pp; English.

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; x = C=O, when the R-X group is attached to the Verminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is COOH or CONH2; and R = 2-18C aikyl or alkoxy, 2-14C aikylenyl containing one or CONH2; and R = 2-18C aikyl or alkoxy, 2-14C aikylenyl containing one or CONH2; and R = 2-18C aikyl or alkoxy, 2-14C aikylenyl containing one or coubstituted with a 1-5C straight or branched chain phenyl optionally monosubstituted with a 1-5C straight or branched chain phenyl optionally monosubstituted with a 1-5C straight or branched chain of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superiamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the call death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma-leukemia 2 (Bd1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 unction in particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that cancer includes prostate, coloretal, gastric, nor-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for treating discussed apontors of a neuroblastoma and non-small and non-small and non-small apontors.
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Claim 18; Page 19; 74pp; English.

X The invention relates to a peptide conjugate having the formula:

CC (R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the vide chain of the peptide where to the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide where the side chain functional group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally or convenientated with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AbB37001-B3708 represent examples of the peptide portion of the conjugate. The peptide corresponding to amino acids 72-97 of the BH3 domain of the conjugate. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell apphoma/leukemia 2 (Bcl-2) mediated blockage of a poptosis in cancer cells of a subject, or for reversing B cell apphoma/leukemia 2 (Bcl-2) mediated blockage of unction. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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Sequence 28 AA;
Ouerv Match 95.2%;

Query Match 95.2%; Score 138; DB 21; Length 28; Best Local Similarity 100.0%; Pred. No. 3.2e-14; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 27, Appl
Sequence 27, Appl
Sequence 4656, Ap
Sequence 31348, A
Sequence 19594, A
Sequence 19594, A
Sequence 32466, A
Sequence 31488, A
  Sequence 3, Appli
Sequence 1, Appli
Sequence 40, Appl
Sequence 18296, A
                                                                                                                                                                  Sequence 5164, Ap Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORMATION:
APPLICANT: KORSMEYER, Stanley J.
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bel.*XBel.-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/333,565
FILING DATE: 31-OCT 1994
CLASSIFICATION: 435
ATTORNEY/AGRET INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
US-09-388-774-3

US-09-546-1153-1

US-08-252-991A-4206

US-09-522-991A-4206

US-09-551-656-27

US-09-552-991A-31348

US-09-252-991A-31348

US-09-252-991A-31348

US-09-252-991A-31348

US-09-252-991A-31348

US-09-252-991A-31458

US-09-252-901A-31458

US-09-252-901A-31458

US-09-252-901A-31458

US-09-255-103-4

US-09-255-103-4

US-09-255-103-4
                                                                                                                                                                                                                         PCT-US94-08449A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 15726A-000700 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400 TELEPHAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08333565; Patent No. 5622852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
    COMPUTER READABLE FORM:
  ZIP: 94301
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US-08-333-565-2
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Gaps

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100.0%; Score 145; DB 1; Length 204; 100.0%; Pred. No. 1.4e-14; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 27; Conservative

Seguence Sequence Sequence

/note= "Deduced amino acid sequence of mouse BAD."

) OTHER INFORMATION: OTHER INFORMATION: US-08-333-565-2

TOPOLOGY: linear MOLECULE TYPE: protein

NAME/KEY: Protein

LOCATION:

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
SOFTRM: PC-DOS/MS-DOS
SOFTRME: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 145; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-14; Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: HOWELL & BAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
               7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 NLWAAQRYGRELRRMSDEFEGSFKGLP 166
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                                                                                                                                                                                                                        APPLICATION:
FILING DATE:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFRENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
TYPE: amino acids
HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ. ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              % Sequence 12, Application US/08733505A; Patent No. 5856445; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
HOWELL
       STREET: 7/35 CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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63105
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                                                                    COUNTRY: US
ZIP: 63105
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-733-505A-1
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BELLE SCHEME SCHEMED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                  APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BC1-x/Bc1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGILATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCES: 59
CORRESPONDENCES: COMMISSION: ADDRESSER: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 145; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-14; Matches 27; Conservative 0; Mismatches 0;
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1 NIWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of mouse BAD
                                                                                                                         Sequence 2, Application US/08661479 Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: 0. COTHER INFORMATION: 0. OTHER INFORMATION: 0. US-08-661-479-2.
                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-733-505A-1
                                                                                        RESULT 2
US-08-661-479-2
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Sequence 3, Application US/08717123
Fatent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 PORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
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APPLICATION NUMBER: US/08/717,123 FILING DATE: 20-5P-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Petchtin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 965
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-5092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.(
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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APPLICANT: KORSMEYER, STANLEY J.

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SCERNE SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSE: HOWELL & HAFERKÂMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI
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                                                                                                                                                                                    Length 204;
                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OCMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PartentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                    ch 100.0%; Score 145; DB 2; Similarity 100.0%; Pred. No. 1.4e-14; 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 NIWAAQRYGRELRRMSDEFEGSFKGLP 166
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US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 204 amino acids
amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-733-505A-13
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Best Local Similarity
Matches 27; Conserv
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Matches 27; Conserv
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US-08-733-505A-13
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                                                                                                                                                                                                                                                                                                                                                                                     Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE: 105/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: #35
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbeal and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                               DB 1.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 120.5; DB 2;
Pred. No. 6.3e-11;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                           Query Match 83.1%; Score 120.5; DB 1; Best Local Similarity 89.3%; Pred. No. 6.2e-11; Matches 25; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-717-123-2; Sequence 2, Application US/08717123; Patent No. 5965703
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELEPHONE: (352) 375-8100
TELEPRAX: (352) 375-8100
TELEPRAX: (352) 375-800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.1%;
89.3%;
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Best Local Similarity 89.3
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-717-123-2
                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92122
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Patent No. 566316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INFUNIONS:
TATLE OF INFUNIONS: 2
CORRESPONDENCE ADDRESS:
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O
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APPLICANT: Horne, William A.
APPLICANT: OlterSourf, Tilman A.
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE FILE REPERENCE: 480140.428D1
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08*16
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%; Score 142; DB 4; Length 204; 96.3%; Pred. No. 4.1e-14; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                    Score 142; DB 2; Length 204;
Pred. No. 4.1e-14;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Galiosaville STRATE: Florida COUNTRY: USA COUNTRY: USA COUNTRY: USA STAME: Florida COUNTRY: USA STAME FORM: MEDIUM TYPE: Floryy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 NLWAAQRYGRELRRWTDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                    1 NIWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                           1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
      P-ID 1929
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APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09375257 Patent No. 6504022
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                    Query Match 97.9%;
Best Local Similarity 96.3%;
Matches 26; Conservative 1
      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
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CORGANISM: Mus musculus
US-09-375-257-3
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                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-375-257-3
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APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Aph, Preeti
APPLICANT: Ocoley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 120.5; DB 3;
Pred. No. 6.3e-11;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIOM TYPE: Diskette
COMPUTER: IBM COMPACTIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                   COMPOTER EADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION NATE:
FILING DATE: Filed Herewith
            SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Dr.
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRWSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
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                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0421 US
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: BILLINGS, Lucy J.,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELEPHONICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09410372
Patent No. 6281334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
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Best Local Similarity 89.3'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 FILING DATE: Filed H
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CORRESPONDENCE ADDRESS:
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LIBRARY: Geneum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: line
IMMEDIATE SOURCE:
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                                                                                                   USA
                                                                                                                  94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                              STATE: CA
                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CLONE: 1
US-08-985-335-7
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CITY: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                           APPLICANT: Yue, Henry
APPLICANT: Ial, Preeti
APPLICANT: Shah, Pureti
APPLICANT: Shah, Pureti
APPLICANT: COTIEY, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEB: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                       ZOUNTKY: USAR
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: The Compartible
COMPUTER: The Compartible
COMPUTER: The Compartible
COMPUTER: The Compartible
CURRENT APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
RIOR APPLICATION NUMBER: 36,749
FILING DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
RETERPONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENOTH: 168 amino acids
TYPE: amino acid
STRANDORMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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                                                                        Sequence 1, Application US/08985335 Patent No. 6080847 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08985335 Patent No. 6080847 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: SYNORAB01
CLONE: 358673
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Matches 25; Conserv
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                                                         US-08-985-335-1
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ORGANISM: Homo sapiens
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-09-410-372-7
                                                                                                                                       Query Match
Best Local Similarity
Watches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-375-257-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yue, Henry
APPLICANT: Jal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-845-4166
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                    PF-0421 US
    PRIOR APPLICATION DAMAS

APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/ACRETY INCRMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421
FELECOMGUNICATION INFORMATION:
TELECOMGUNICATION INFORMATION:
TELECOMGUNICATION INFORMATION:
TELECOMGUNICATION INFORMATION:
TELECOMGUNICATION: 1:
FELECOMGUNICATION OF 15.
SEQUENCE CHRACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: Inmeaning acid
STRANDEDNESS: Single
TYPE: LENGTH: SOURCE:
LIBREANT: SUNORABOI
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/985,335
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-410-372-7
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Gaps
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  Length 168;
                                                                                                                                                                                                                                                                                                                              APPLICANT: COLERACY, William A.
APPLICANT: Oltersdorf, Tilman
APPLICANT: Oltersdorf, Tilman
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140, 420D1
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 2
LENGTH: 168
                                               Indels
  DB 3;
83.1%; Score 120.5; DB 3 ilarity 89.3%; Pred. No. 6.3e-11; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 15, 2003, 17:45:05 Job time : 14.0786 secs
                                                                                                                          103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                            1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                      US-09-375-257-2
; Sequence 2, Application US/09375257
; Patent No. 6504022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.1
Best Local Similarity 89.3
Matches 25; Conservative
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(without alignments)
184.034 Million cell updates/sec
                                                                                                                                                                                                          September 15, 2003, 17:25:56; Search time 21.4071 Seconds
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/cgn2_6/prodate/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/prodate/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/prodate/1/pubpaa/US02_NEW_PUB.pep:*
/cgn2_6/prodate/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/prodate/1/pubpaa/US10_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
.: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541936 segs, 145912426 residues
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1 NIWAAQRYGRELRRMSDEFEGSFKGLP
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                   Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 147, App Sequence 147, App Sequence 3, Appli Sequence 1, Appli Sequence 214, Appli Sequence 1, Appli Sequence 1, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli
SUMMARIES	US-09-922-378-3 US-10-066-179-3 US-09-894-657-1 US-09-894-657-7 US-10-66-179-2 US-10-065-261-258 US-10-174-105A-147 US-10-174-105A-147 US-10-092-750-1 US-10-092-750-1 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241 US-10-092-750-241
DB	240004440440 40000440404
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s Query Match	0.000000000000000000000000000000000000
Score	10201 10201 10201 10200
Result No.	2 8 4 8 9 7 8 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 8

Sequence 153, App

10 US-09-984-198-153

852

31.4

45.5

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Sequence 4, Appli Sequence 2, Appli Sequence 16, Appli Sequence 16, Appl Sequence 13, Appl Sequence 435, Appl Sequence 435, Appl	4,0000000	20,27,000,000	Sequence 165, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 62, Appli
US-10-199-869-4 US-10-143-002-2 US-10-325-891-2 US-09-903-190-160 US-10-121-757B-12 US-09-738-933-435	S-10.144-649A-4 S-10-102-806-64 S-09-794-715A-8 S-10-286-581-8 S-10-046-924-8	50.24.21.21.21.21.21.21.21.21.21.21.21.21.21.	US-09-981-752A-248 US-09-934-455-162 US-09-149-045-2 US-10-166-359-2 US-10-166-37-2 US-10-166-37-2 US-10-184-722-3 US-10-184-722-3 US-10-184-722-3 US-10-184-722-3
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### ALIGNMENTS

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Gaps
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                                   Sequence 3, Application US/09922378
Fatent No. US20200037869A1
GENERAL INFORMATION:
APPLICANT: HORNE, William A.
APPLICANT: Oltersdorf, Tilma A.
TITLE OF INVENTION: HUGAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILLE REPERENCE: 480140,428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BED POLYBEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 142; DB 9; Length 20 Pred. No. 2.5e-13; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-066-179-3
: Sequence 3, Application US/10066179
; Publication No. US20020115631Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.9%;
Best Local Similarity 96.3%;
Matches 26; Conservative 1
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Mus musculus
US-09-922-378-3
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RESULT 1
US-09-922-378-3
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83.1%; Score 120.5; DB 9; Length 168; 89.3%; Pred. No. 3.2e-10; Live 0; Mismatches 2; Indels 1
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TITLE OF INVENTION: PROIEINS ASSOCIATED WITH CELL
PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FASTSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGRET INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPOMMUICATION INFORMATION:
TELEPRAX: 650-845-4166
                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-894-657-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                TELEPHONE: 650-855-0555
TELEPAK: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09894657; Patent No. US20020098569Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: SYNORAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yue, Henry
Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 89.3 es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: 358673
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US-09-894-657-7
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09922378;
Patent No. US20020037869Al
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: OlterSodrf, Tilman
TITLE OF INVENTION: ACIDS AND METHODS. ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERBYCE: 480140.428D3
CURRENT PILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 2.
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 168;
                                                                                                                                                                                                              Query Match
97.9%; Score 142; DB 14; Length 204;
Best Local Similarity 96.3%; Pred. No. 2.5e-13;
Matches 26; Conservative 1; Mismatches 0; Indels
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Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.1%; Score 120.5; DB 9
89.3%; Pred; No. 3.2e-10;
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                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 204
                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09894657
Patent No. US20020098559A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READMBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yue, Henry
Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.1
Best Local Similarity 89.3
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-09-922-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-922-378-2
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Gaps ÷ Page 3

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APPLICANT: Cell Signaling Technology, Inc.,
APPLICANT: Cell Signaling Technology, Inc.,
APPLICANT: ZHAN, Hui
APPLICANT: ZHAN, Yi
APPLICANT: TAN, Yi
APPLICANT: TAN, Yi
APPLICANT: TAN, Yi
APPLICANT: TAN, Yi
TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEING MOTIF-SPECI:
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHI
FILE REPREBAGE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US/10/174,105A
CURRENT APPLICATION NUMBER: US/09/148,712
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 193
SOFTAME: PATENT PATENT NOS: 193
SOFTAME: PATENT PATENT NOS: 193
SOFTAME: PATENT PATENT NOS: 193
SOFTAME: PATENT PATENT NOS: 193
SOFTAME: PATENT PATENT NOS: 193
SOFTAME: LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : LOCATION: (8)..(8) ; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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     FEATURE:
OTHER INFORMATION: Description of Unknown Organism: TOX peptide
                                                                                                                                               ò
                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
Guegler, Karl J.
Patterson, Chandra
TITLE OF INVENTION: GROWIH-ASSOCIATED TRYPSIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.0%; Score 71; DB 15; I
100.0%; Pred. No. 0.00058;
tive 0; Mismatches 0;
                                                                                               Score 114; DB 15;
Pred. No. 4.1e-10;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSBE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                           1 NIWAAQRYGRELRRMSDEFVDSFK 24
                                                                                                                                                                                               1 NLWAAQRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                ; Sequence 147, Application US/10174105A; Publication No. US20030068652A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09828423
Patent No. US20020099178A1
GENERAL INFORMATION:
                                                                                               Query Match 78.6%;
Best Local Similarity 91.7%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GRELRRMSDEFEGS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GRELRRMSDEFEGS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
LOCATION: (8)..(8
                                                                                                                                                                                                                                                                                                                                            US-10-174-105A-147
                                               US-10-059-261-258
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                                                                                                  Query Match
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APPLICANT: BELMAN, IENA
APPLICANT: BELMAN, JEAN-POY, ETTENNE DANIEL FRANCOIS
APPLICANT: JACOTOY, ETTENNE DANIEL FRANCOIS
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
TITLE OF INVENTION: PUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
TITLE OF INVENTION: (PPPC)
TITLE OF INVENTION: (PPPC)
TITLE OF INVENTION: (PPPC)
TITLE REFERENCE: 03495-0216
CURRENT APPLICATION NUMBER: 05/265,594
PRIOR FILING DATE: 2002-08-29
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PATENTION OS: 325
SOFTWARE: PATENTIN VET. 2.1
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Sequence 2, Application US/10066179

Sequence 2, Application US/10066179

Publication No. US20020115631A1

GENERAL INFORMATION:

APPLICANT: HORNE, William A.

TILLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REPERENCE: 480140.428C1

CURRENT APPLICATION NUMBER: US/10/066,179

CURRENT FILING DATE: 2002-02-01

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 83.1%; Score 120.5; DB 14; Length 168; Best Local Similarity 89.3%; Pred. No. 3.2e-10; Matches 25; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                          Length 168;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                          Score 120.5; DB 9
Pred. No. 3.2e-10;
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  103 NIWAAQRYGRELRRMSDEFVDSFKKGLP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NLWAAQRYGRELRRMSDEFVDSFKKGLP 130
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                                                                                                                                                                                                                                                                                                                                                                                       1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                            CLONE: 1683637
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 258, Application US/10059261
Publication No. US20030077826A1
GENERAL INFORMATION:
                    SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       83.1%;
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                      LIBRARY: GenBank
                                                                                                                                                                                                                                                                                          Query Match 83.1
Best Local Similarity 89.3
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                             IMMEDIATE SOURCE:
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LENGIH: 25
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Sequence 1077, Application US/10238075; Publication No. US20030148324A1; CENERAL INFORMATION: APPLICANT: I.N.S.E.R.M.
TAPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isc; TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                        Sequence 1, Application US/10092750
; Sequence 1, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION
; APPLICANT: Hamond, Philip W.
; APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
; FILE REFERENCE: 50036/05002
; CURRENT APPLICATION NUMBER: US 60/274,526
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SED ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%; Score 47; DB 15; Length 35; 45.5%; Pred. No. 5.1;
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"Sequence 241, Application US/10092750
"Publication No. US20030032157A1
"GENERAL INFORMATION:
"APPLICANT: Alpin, Julia
"APPLICANT: Alpin, Julia
"APPLICANT: Wright, Martin C.
"TILE OF INVENTION: Polypeptides Interactive with BCL-X1
"FILE REFERENCE: 50036/050002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 241
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.4%; Score 47; 45.5%; Pred. No.
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  108 ERWGGDLRRMRDEADG 123
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Best Local Similarity 45.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-092-750-241
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US-10-238-075-1077
                                                                      RESULT 11
US-10-092-750-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
LENGIH: 35
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20;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: WORD PREFECT 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.5%; Score 50; DB 15; Best Local Similarity 56.2%; Pred. No. 12; Matches 9; Conservative 4; Mismatches 3
                                                                                                                                                                                                                                  FILING DATE: <Unknown>
ATTORNEY/AGENY INPORADITON:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REPERBRUGE-ZPOCKET NUMBER: PF-0505 US
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.6%; Score 53; DB Best Local Similarity 33.3%; Pred. No. 20; Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OMURA, SATOSHI
APPLICANT: OMURA, SATOSHI
APPLICANT: INEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAWA, HROSHI
APPLICANT: SHIBA, TADAVOSHI
APPLICANT: SARAKI, YOSHIVUKI
APPLICANT: SARAKI, YOSHIVUKI
APPLICANT: HATORI, MASAHIRA
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/388,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GENEBANK
CLONE: 9133985
SEQUENCE DESCRIPTION: SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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US-10-156-761-9145
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US-10-156-761-9145
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APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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                      Length 852
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                  Score 45.5; DB 9;
Pred. No. 2.4e+02;
5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 DIWSTYLTKFIARYGGRKLERARDLFEQALDGCP 585
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                                                                                                             1 NLWAA-----QRY-GRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastEn for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 41,386
REFERENCE/COCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 15, 2003, 17:47:52 Job time: 21.4071 secs
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/081,385
FILING DATE: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               Sequence 153, Application US/09984198 Patent No. US20020106679A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELBERAY: 650.
TELEFRAY: 650.
TELEER: 706141
; INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
""DR: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153:
                    Query Match 31.4%;
Best Local Similarity 35.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-09-984-198-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Wu, Frank
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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STATE:
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Patent No. US200200301243A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granager, GA.
APPLICANT: Granager, GA.
TITLE OF INVENTION: Factor Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of USe Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                  Query Match 31.7%; Score 46; DB 12; Length 68
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING DATE:
CLASSIFICATION:
PERFORM PERFORMATION:
PRIOR PAPELICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 22000-20577.21
                  CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEQ ID NO 1077
                                                                                                                                                                                                                                                                                                                                                                                               :||||| | :: |: : | ||| || 634
                                                                                                                                                                                                                                                                                                                                                                         2 LWAAQRYGRELRRMSDEFEGSFKGL 26
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APPLICATION NUMBER: 09/081,385
FILING DATE: 08/964,747
APPLICATION NUMBER: 08/964,747
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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REGISTRATION NUMBER: 41,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
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ZIF: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: amino acid
; STANDEDNESS: single
; TOPOLOGY: linear
US-09-752-639-153
FILE REFERENCE: BLANDINE
                                                                                                                                                                                                                                         US-10-238-075-1077
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US-09-752-639-153
                                                                                                                                                                           682
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STATE:
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(without alignments)
213.708 Million cell updates/sec
                                                                                                                                 September 15, 2003, 17:18:16; Search time 12.15 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                             283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                   1 NLWAAQRYGRELRRMSDEFEGSFKGLP
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                        US-09-544-664-3
                                                                                                                                                                                                                                                Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR\_76:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

# SUMMARIES

Description	bad protein - mous	inter-alpha-ulypsi inter-alpha-inhibi	hypothetical prote	inter-alpha-trypsi	2-dehydro-3-deoxy-	floral homeotic pr	spermidine/putresc		endonuclease VIII		hypothetical prote	endonuclease VIII,	conserved hypothet	Ig kappa chain - h	annexin P35 - maiz	transforming prote	oxidoreductase, so	threonine synthase				hypothetical prote	annexin P33 - maiz	Antho-RFamide prec	hypothetical prote	probable polyamine	alkaline proteinas	hypothetical prote
ai	in u	S54354	D70760	IYHU2	S38185	A42095	C84338	A96753	A64807	A85572	C90721	AD0590	E83517	S40376	T02975	C36365	F72289	T08545	B81287	G82308	F82668	B96695	T02961	A44308	T09486	T35440	C98318	T24806
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% Query Match	00	42.1	Q	S	35.9	IJ	34.5	34.5	33.8	33.8	33.8	33.8	33.8	33.4	33.4	33.1	33.1	33.1	32.8	32.4	32.4	32.4	32.1	32.1	32.1	31.7	31.7	31.7
Score		09	23	53	52	51	20	20	49	49	49	49	49	48.5	48.5	48	48	48	47.5	47	47		46.5		46.5	46	46	46
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DNA-directed RNA p	conserved hypothet	probable transfera	neuropeptide Pol-R	probable transmemb	Antho-RFamide neur	hypothetical prote	NADH dehydrogenase	chlorocruorin chai	conserved hypothet	conserved hypothet	potassium channel	xo dund uoi mnipos	oxaloacetate decar	oxaloacetate decar
A81393	669510	E81148	S43852	E83337	A39172	C71473	G83314	859899	F83201	H95406	JC5920	B44465	AB0509	AE0909
77	1 (1	N	7	7	7	7	~	~	7	N	~	~	~	7
1378	261	263	287	328	334	562	902	165	295	346	513	591	591	165
31.7	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.0	31.0	31.0	31.0	31.0	31.0	31.0
91	. 10	5.5	5.5	5.5	5.5	45.5	45.5	45	45	45	45	45	45	45
46	+ 4	4	4	4	4	4	4							

## ALIGNMENTS

C. Species: Mesocricetus auratus (golden hamster)
C. Species: Mesocricetus auratus (golden hamster)
C. Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000
C. Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000
C. Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000
R. Maketani, T.; Suzuki, Y.;
Mammoto, T.; Sinohara, H.
A. Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs sin inhibitor heavy chain family.
A. Reference number: JC5574; MUID:97420688; PMID:9276673
A. Moccasion: JC5575
A. Molecule type: mRNA
A. Residues: 1-946 < NAKA
A. Residues: 1-946 < NAKA
A. Residues: 1-946 < NAKA
A. Molecular source: 11ver
A. Molecular source: 11ver
A. Molecular source: 11ver
A. Molecular source: 11ver
A. Molecular source: 11ver
A. Molecular source: 11ver
A. Molecular source: 11ver
A. Molecular source: 11ver

A; Experimental Source: 11ver
A; Accession: 104485
A; Molecule type: protein
A; Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C; Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important role for panceatic cancer.
C; Superfamily: inter-alpha-trypsin inhibitor component II
F;261-264,717-916/Disulfide bonds: #status predicted

2b1-2b4//1/-91b/Disulfide Donds: #Status predicted
Ouery Watch
42.1%; Score 61; DB 2; Length 946;
Best Local Similarity 37.0%; Pred. No. 1;

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A.Map position: 10p15-10p15
C; Superfamily: inter-alpha-trypsin inhibitor complex component II
C; Superfamily: inter-alpha-trypsin inhibitor complex component II
C; Superfamily: inter-alpha-trypsin inhibitor complex serine proteinase inhibitor (**Reywords: carboxyglutamic acid; glycoprotein; bredicted (**SIG)*
F; 1-18, Domain: signal sequence **status predicted (**SIG)*
F; 15-569* Product: inter-alpha-trypsin inhibitor heavy chain 2 **status predicted (**Mar)*
F; 15-69* Product: inter-alpha-trypsin inhibitor heavy chain 2 **status predicted (**Mar)*
F; 16, 46, Finding site: carbohydrate (**Asn) (covalent) **status predicted
F; 18, 671, Finding site: carbohydrate (**Asn) (covalent) **status predicted
F; 282, 283, Modified site: gamma-carboxyglutamic acid (Glu) **status predicted
F; 421, 422, 423, Finding site: calcium (**Asp.** dly, Asp) **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S09064
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
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A; Moseduces 384-673.74', 675-704,'S',706-728,'D',730,'A',732-766 <SA2>
A; Cross references: GB:M33033; NID:g186589; PIDN:AAA59195.1; PID:g186590
R; Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
B.B.O. Cohen. 264, 15975-15981, 1989
A; Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre
A; Reference number: A92736; WUID:89380192; PMID:2476436
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A;Residues: 55-74 <ENG>
R;Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fou
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolat
A;Reference number: S28928; MUID:93039735; PMID:1384548
                                                                                                                                                                                                                                                                                                                                               A) Experimental source: liver
A;Note: part of this sequence, including the amino end of the mature protein, was con
A;Note: part of this sequence, including the amino end to produce the mature protein
A;Note: due to a double frameshift, the nucleic acid sequence of codons 363-372 is in
A;Note: in one clone, a T is lacking from codon 716; this clone could code for a prot
R;Schreitmueller, T.; Hochstrasser, K.; Reisinger, P.W.M.; Wachter, E.; Gebhard, W.
A;Title: CDNA cloning of human inter-alpha-trypsin inhibitor discloses three differen
A;Reference number: S09064; MUID:88024442; PMID:3663330
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Bochemistry 33, 7423-7429, 1994
A:Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable co
A:Reference number: A53642; MUID:94271799; PMID:7516184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: Inter-alpha-trypsin inhibitor is a complex of three proteins, each derivin C;Comment: This protein is a heterodimer of heavy and light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. Hoppe-Seyler 369(Suppl.), 15-18, 1988
A;Title: Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy
A;Reference number: S00632; NUID:89076497; PMID:2462430
A;Accession: S00632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 384-673, A, 675-704, 'S', 706-728, 'D', 730, 'A', 732-865 <SAL>
A; Residues: 384-673, A, 675-704, 'S', 706-728, 'D', 730, 'A', 732-865 <SAL>
A; Experimental source: 11 yer
A; Experimental source: 11 yer
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      precursor of
      the
A;Title: Complementary DNA and derived amino acid sequence of A;Reference number: S00346; MUID:88152237; PMID:2450046
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A; Residues: 55-64 <MAL>
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                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-946 <GEB>
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                                                                                                                            A; Accession: S00346
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C; Species: Mycobacterium tuberculosis

C; Species: Mycobacterium tuberculosis

C; Accession: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-oct-1999

C; Accession: D7060

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanris, D.; Gordon, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.

A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Reference number: A70500; MUID:98295997; PMID:9634230

A; Reference number: A70500; MUID:98295997; PMID:9634230

A; Ratus: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DMY

A; Molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inter-alpha-inhibitor H2 chain - mouse
C;Species: Was musculus (house mouse)
C;Species: Was musculus (house mouse)
C;Species: Was musculus (house mouse)
C;Accession: 554354
R;Chan, P.; Risler, J. L.; Raquenez, G.; Salier, J.P.
B;Chan, J. 306, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:
A;Reference number: S54353; MUID:95194326; PMID:7534067
A;Accession: S54353; MUID:95194326; PMID:7534067
A;Accession: S54353; MUID:95194326; PMID:7534067
A;Accession: S54354
A;Accession: S54354
A;Accession: S54354
A;Accession: Disperimenty
A;Molecule type: MRNA
A;References: EMBL:X70392; NID:9695633; PIDN:CAA49842.1; PID:9695634
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e1299911;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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      Indels
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                                                                                                                                                                                                                                      NVWIVELQGMRFLHVPDTFEGHFQGVP 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                      1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
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            Conservative
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      10;
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Cincession: C84338
Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky F.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Fraitas, T. 2.
Jung, K.H.; Alam, M.; Fraitas, T. 2.
Jung, K.H.; Alam, M.; Fraitas, T. 2.
Jung, K.H.; Alam, M.; Fraitas, T. 2.
Jung, M.J.; Dower, A.D.; Ebhardt, H.; Lowe, T.M.; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Ower, A.D.; Ebhardt, H.; Lowe, T.M.; A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Ower, A.D.; Ebhardt, H.; Lowe, T.M.; A; Reference numbers a84160; MUID:20504483; PMID:11016950
A; Accession: C84338
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Ara A;Reference number: $52633; MUID:95036018; PMID:7948893
A;Accession: $52633
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A;Reference number: 224469
A;Accession: T47593
                                                                                                                                                                                                                                                      A42095
floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
NA1ternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
(Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42095, S25633; T47593
B;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Call 68, 683-697, 1992
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and iA;Reference number: A42095, MUID:92154682; PMID:1346756
A;Accession: A42095
A;Accession: A42095
A;Accession: A2305
A;Accession: A2305
A;Accession: A42095
A;Accession: 
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
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A;Experimental source: cultivar Columbia; BAC clone T12E18
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A;Note: T12E18.30
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Okamoto, H.; Yano, A.; Shiraishi, H.; Okada, Plant Mol. Biol. 26, 465-472, 1994
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                     OLEAAQEYALRIKKLSDELKG 100
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Best Local Similarity 44.4%;
Matches 12; Conservative
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A, Residues: 1-63 < OKA>
A, Cross-references: GB:D21125
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A, Residues: 1-370 (ALG)
A, Accession: 0.9410.
A, Accession: 0.9410.
A, Accession: 0.9410.
A, Accession: 0.9410.
A, Accession: 0.9410.
A, Accession: 0.940.
A, Residues: 1-204
Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosi A, Recience number: 0.00
A, Recience number: 0.00
A, Accession: 0.0032
A, Molecule type: DNA
A, Residues: 1-204
A, Besterences: EMBL:X61107
A, Residues: 1-204
A, Bacteriol: 175, 548-558, 1993
A, Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifuncti A, Reference number: A48651; MUID:93374850; PMID:8366040
A, Residues: 32-370
A, Residues: 32-370
A, Residues: 32-370
A, Residues: 32-370
A, Residues: 35-370
A, Cross-references: GB:X61107
A, Residues: 35-370
A, Cross-references: GB:X61107
C, Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitelater alwaes: 3 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 Jecoxy 2 
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A;Residues: 1-370 <ALJ>
A;Residues: 1-370 <ALJ>
A;Cross-references: EMBL: 236118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR2496
R;Aigle, M.; Baclet, M.C.; Barthe, C.; Bitcau, N.; Crouzet, M.; Doignon, F.
A;Reference to the Protein Sequence Database, August 1994
A;Reference number: 546940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces or N;Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
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A;Cross-references: SGD:S0000453; MIPS:YBR249c
A;Cross-references: SGD:S0000453; MIPS:YBR249c
A;Cross-references: CGD:S0000453; MIPS:YBR249c
C;Function: aldehyde-lyase; carbon-carbon lyase
A;Pathway: aromatic amino acid biosynthesis; shikimate pathway
A;Pathway: aromatic amino acid biosynthesis; shikimate pathway
A;Coperfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C;Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase;
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Score 53; DB 1; Length 946;
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                                                     Pred. No. 15;
5; Mismatches
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Pred. No. 8
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47.6%;
          36.6%;
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Best Local Similarity 47.6
Matches 10; Conservative
     Query Match
Best Local Similarity 33.33
Matches 9; Conservative
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A; Molecule type: DNA
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecules 1-263 <STO>
A;Rosidues: 1-263 <STO>
A;Cross-references: GB:AE005174; NID:g12513625; PIDN:AAG55037.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
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C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
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A: Mitle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein nei [imported] - Escherichia coli (strain O157:H7, substrain EDL
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
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A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                    Length 263;
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                                    Score 49; DB 2;
Pred. No. 16;
; Mismatches 7
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C;Superfamily: formamidopyrimidine-DNA glycosidase
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3; Mismatches
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Pred. No. 1
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GPEIRRAADNLEAAIKGKP 22
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A; Residues: 1-263 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable threonine synthase [imported] - Arabidopsis thaliana probable threonine synthase [imported] - Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A96753 C;Accession: A
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Cypecies: Escherichia coli

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Cypecies: Escherichia coli

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Ryblattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC

A.; Rose, D.J.; Mau, B.; Shao, Y.

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Accession: A64807

A; Status: nucleic acid sequence not shown; translation not shown
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A; Residues: 1-263 CBLATD
A; Cross-references: GB:AE000174; GB:U00096; NID:g1786920; PIDN:AAC73808.1; PID:g1786932;
A; Experimental source: strain K-12, substrain MG1655
A; Cross-references: cource: strain K-12, substrain MG1655
A; Gpetics:
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O
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                       A;Cross-references: GB:AE004437; NID:g10581314; PIDN:AAG20071.1; GSPDB:GN00138 C;Genetics:
A;Gene: potA2
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C;Genetics:
A;Gene: F3N23.1
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                                                                                                                                                                   Length 374;
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ed. No. 16;
Mismatches 2
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Pred. No. 23;
7; Mismatches
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Pred. No.
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76.9%;
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
A; Residues: 1-374 <STO>
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Gaps

11;

o, DB 2;

Score 48.5; DB Pred. No. 9.3; 1; Mismatches

Length 134; Indels

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A;Cross-references: EMBL:X72486; NID:g441440; PIDN:CAA51154.1; PID:g441441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-113/Pommain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                  3 WAAQRYGRELRRM-----SDEFEGSFKG 25
                                                                                                                                                                                                                                                                                                                         Search completed: September 15, 2003, 17:27:01 Job time : 13.15 secs
                                                                                                                                                           33.4%;
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004535; GB:AE004031; NID:99946936; PIDN:AAG04420.1; GSPDB:GN001
A;Experimental source: strain PA01
                                                                                       C) Accession: A00590
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connection, P.; Cronin, A.; Davis, P.; Pavies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica servy A; Reference number: AB0502; MUID:21334947; PMID:11677608
A; Reference number: AB0502; MUID:21334947; PMID:11677608
A; Accession: AD0590
A; Arealuminary
A; Molecule type: DNA
A; Molecule type: CRAPA
A; Residues: 1-263 cPAR>
A; Residues: 1-263 cPAR>
A; Cross-references: GB:AL513382; PIDN:CAD05190.1; PID:916501960; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa () Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83517
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; Length 263;
Pred. No. 16;
3; Mismatches 7; Indels
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Pred. No. 28;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: formamidopyrimidine-DNA glycosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GPEIRRAADNLEAAIKGKP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 GRELRRMSDEFEGSFKGLP 27
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Best Local Similarity 55.65
Matches 10; Conservative
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Best Local Similarity
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A; Residues: 1-453 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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September 15, 2003, 17:16:55; Search time 6.36429 Seconds (without alignments) 199.507 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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145
1 NIWAAQRYGRELRRMSDEFEGSFKGLP 27
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Maximum Match 100%
Listing first 45 summaries
                                                                            using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	061337 mus musculu 035147 rattus norv 092934 homo sapien P9729 mesocnicetu 061703 mus musculu P19823 homo sapien P3449 araccharomyc P35632 arabidopsis 082942 indoddendro 062994 rhododendro 062994 rhododendro 062992 ledum palus 062992 ledum palus 062994 rhododendro 082905 escherichia p56465 escherichia 082906 salmonella 094403 pseudomonas P22280 rhizomucor 029008 thermotoga 094019 sarabidopsis 04351 homo sapien 019994 anthopleura 029900 mus musculu 099900 rattus norv 099802 drosophila 04129 polyorchis 041133 calliactis 041759 homo sapien 099009 liseturia 090009 liseturia 090009 liseturia 0900000000000000000000000000000000000
SUMMARIES	BAD_MOUSE BAD_RAT BAD_RAT BAD_RAT BAD_RAT ITHE_MOUSE ITHE_MOUSE APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST APS_G_YEAST THRC_SOLTU FHRC_SOLTU FHRC_SANTE FHRT_ANTEL YARL_ANTEL YARL_AN
DB	
Length	200 100 100 100 100 100 100 100
% Query Match	0001 0000
Score	10 44 44 44 44 44 44 44 44 44 44 44 44 44
Result No.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Q9uix4 homo sapien Q03030 salmonella	P13187 klebsiella Q13049 homo sapien	P05886 simian immu	Q18823 caenorhabdi	Q9p0j0 h nadh-ubiq	P33602 escherichia	P33900 salmonella	O54918 mus musculu		P27757 simian immu
KCG1_HUMAN DCOA_SALTY	DCOA_KLEPN HT2A_HUMAN	ENV_SIVAT	LML1_CAEEL	NB6M_HUMAN	NUOG_ECOLI	NUOG_SALTY	BIM_MOUSE	BIM_RAT	ENV_SIVA1
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513	595 653	865	1535	143	907	907	196	196	768
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45 45	4 5 5 5	45	45	44.5	44.5	44.5	44	44	44
34	36	38	39	40	41	42	43	44	45

## ALIGNMENTS

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SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D^\prime Agata \ V. , Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                    S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION; INTERACTS WITH
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
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PKB).
PKB).
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16-0CT-2001 (Rel. 40, Last educe update)
16-0CT-2003 (Rel. 40, Last annotation update)
28-FFB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
                                                                                                                                                                                                                                                                                                                         100.0%; Score 145; DB 1; Length 204; 100.0%; Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
          major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                PKA AND
                                                                                                                                                                                                                                                                                                    6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                           S->A: NO PHOSPHORYLATION.
                                                                                                                                                                                                                            PKA 7
                                                                                                                                                                                                                           PHOSPHORYLATION (BY PHOSPHORYLATION (BY PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6) (Bcl-xL/Bcl-2 associated death promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA.
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                NIMAAQRYGRELRRWSDEFEGSFKGLP 166
                                                                                                                                                                                                                                                                                                                                                                   1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                            BCL-X(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurosci. Lett. 243:137-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=98194755; PubMed=9535132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21109372; PubMed=11161472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Ovary;
MEDLINE-98034386; PubMed-9369453;
                                                                                                                                                           HSSP, Q92934; 1G5J.
MGD: MGT:1096330; Bad.
InterPro; IPR000712; Bc12_BH.
PROSITE; P601259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                     22080 MW;
                                                                                                                                      EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                    Similarity 100.
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                161
112
1136
1136
1136
                                                                                                                                                    PIR; A55671; A55671.
                                                                                                                                                                                                                                                                                                     204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain."
                                                                                                                                                                                                                           112
136
155
112
136
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                                                                                                                                                                                                                                                                                                      SEQUENCE
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MOD_RES
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                                                                                                                                                                                                                                                           MUTAGEN
                                                                                                                                                                                                                                                                     MUTAGEN
                                                                                                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAD.
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Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

Their interaction with Bol-w in sympathetic neurons.";

Hol. Cell. Neurosci. 17:97-106(2001).

Cell. Neurosci. 17:97-106(2001).

Holding to Bol-x(L), Bol-2 and Bol-w, thereby affecting the level of their ordinarization of these proteins with BAX. Can reverse the of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bol-x(L), but not that of Bol-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

Cell, Bol-2 and Bol-w. Also binds protein S100AlO. The Service SUDSILIATS phosphorylated form binds 14-3-3 proteins.

Cell, Bol-2 and Bol-w. Also binds protein S100AlO. The Service SUDSILIATE LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS. NO EFFECT ON HETERODIMERIZATION
WITH BELLS NOR WITH PROTEIN P11.
SDAGGR -> ERRGRK (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S->A: NO EFFECT ON HETERODIMERIZATION WITH 14-3-3 PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
PHOSPHORYLATION
PHOSPHORYLATION (BY PKA AND PKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId-VSP_000534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=035147-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01259; BH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF003523, AAC5374.1; -. BMBL, AF031227, AAC15100.1; -. EMBL, AF279910, AAF91427.1; -. EMBL, AF279911, AAF91428.1; -.
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22228 MW;
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InterPro; PR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSF
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205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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STRUCTURE BY NMR OF 103-127.
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TATANGE-LUNG;

TATANGE-LUNG;

RADINE-LUNG;

RADINE-LUNG;

RADINE-LUNG;

RADINE-LUNG;

RADINE-LUNG;

RADISCHUI S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RADISCHUI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bath R.K.,

RADISCHUI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bath R.K.,

RADISCHUI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bath R.K.,

RADISCHUI S.F., Zeeberg B., Buetow K.H., Subin G.M., Hong L.,

RADISCHUI S.F., Zeeberg B., Parmer A.A., Rubin G.M., Hong L.,

RADISCHUI S., Soares M.B., Bonaldo M.F., Carannof P., Prange C.,

RADISCHUI T.B., Toshiyuki S., Carninci P., Prange C.,

RADISCHUI T.B., Toshiyuki S., Carninci P., Prange C.,

RADISCHUI S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RADIALON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.H.,

RADIALON D.K., Wadny D.M., Sodergren E.J., Lu X., Gibbs R.H.,

RADIALON B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RODIGUEZ A.C., Grimwood J., Schmutz J., Myers R.M.,

RODIGUEZ A.C., Grimwood J., Schmutz J., Myers R.M.,

RODIGUEZ A.C., Grimwood J., Schmutz J., Myers R.M.,

REDISCHUI S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

RODICUL A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yin\ D.X. , Li Z., Huang B., Chen S., Zhou H.; "A human protein that interacts with Bcl-2 and have homology to mouse
                                                                                                                                                                                                                                                                                                                         10-UCT-2001 (Rel. 40, Last sequence update)
BG-SEP-2003 (Rel. 42, Last annotation update)
BG-2-antagonist of cell death (RbD) (BG-2 binding component 6) (BG-XI/BG-2 associated death promoter) (BGL-2 binding component FD RB PD OR BBCG OR BGL2LB.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ottilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G., Chang S., Weeks S., Fritz L.C., Oltersdorf T.; "Dimerization properties of human BAD."; J. Biol. Chem. 272:30866-30872(1997).
                                                                     0;
                        Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97083574; PubMed-8929532; Wang H. -G., Rapp U.R., Reed J.C.; "Bcl-2 targets the protein kinase Raf-1 to mitochondria."; cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Takayama S., Reed J.C.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
                      Score 145; DB 1;
Pred. No. 1.4e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                       168 AA.
                                                                                                                                                 141 NLWAAQRYGRELRRMSDEFEGSFKGLP 167
                                                                                                                    1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND DIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bone marrow;
MEDLINE=98049554; PubMed=9388232;
                                                                                                                                                                                                                                                                                                          092<u>9</u>34; 014803;
01-N07-1997 (Rel. 35, Created)
16-007-2001 (Rel. 40, Last sequ
15-SEP-2003 (Rel. 42, Last anno
                           100.0%;
                                            100.0%;
                                                                          27; Conservative
                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Human)
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                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                       BAD_HUMAN
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).

-!-SUBCELDIAR LOCATION: Outer mitochondrial membrane. Upon phosphorytation, locates to the cytoplasm.
-!-TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-!-DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the BC-2 family.
-!-PTM: Phosphorylated on Ser-75 in response to survival stimuli.
Subsequent phosphorylation on Ser-79 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.

Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: BLONGS TO THE BCL-2 FAMILY.
-!- CAUTION: Ref. 1 sequence differs from that shown due to frameshifts in position 64 and 91.
                                                        Meadows R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PKA AND PKB)
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DOMAIN 110 124 BH3.
MELLINE-21073561; PubMed=11206074;
Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T.,
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> S (in dbSNP:3729933)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAS.
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GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005741, C:mitochondrial outer membrane; N
GO; GO:0005515; F:protein binding activity; NAS.
GO; GO:0008632; P:apoptotic program; TAS.
GO; GO:00086317; P:induction of apoptosis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frid=VAR_015380.
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EMBL; AF021792; AAB72092.1; -
EMBL; AR0315.23; AAB88124.1; -
EMBL; BC001901; AAH01901.1; -
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PROSITE; PS01259; BH3; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-01
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                ij
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97420688; PubMed-9276673;
Makatani T., Suzuki Y., Yamamoto T., Sinohara H.;
Makolecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: I'ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HI, HA OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I'ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I'ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P'ALPHA-LI) OF H3 AND BYM: HEAVY CHAINS ARE INTERINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR O'TERMINAL ASPARTATE (BY
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUNCTION: MAI ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX FROTEIN, INCLUDING THOSE ON CELL SURRACES IN TISSUES TO REGULARE THE LOCALIZATION, SYNHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian hanster urine and plasma.";
J. Biochem. 120:145-152(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                1;
                Indels
Pred. No. 5.5e-11;
                                                                                                                                   946 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITIH FAMILY.
                Mismatches
                                                       1 NLWAAQRYGRELRRMSDEFEGSF-KGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ITH FAMI SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                            Mesocricetus auratus (Golden hamster).
                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97018241; PubMed=8864857;
              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. 122:71-82(1997).
89.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D89286; BAA13939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; DR00587; VII.
InterPro; DR00587; VII.
InterPro; DR002035; VWE_A.
Pfam; PF00092; vwa; 1.
SMART; SM00609; VII; 1.
               Conservative
                                                                                                                                    STANDARD;
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        chain family
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                     Mesocricetus
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                25;
                                                                                                                                    ITH2_MESAU
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                Matches
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                                                                                                                                            INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6N; TISSUE-Liver;
MEDLINE-95194326; PubMed-7534067;
Chan P., Risler J.-L., Raquenez G., Salier J.-P.;
"The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN: INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family in mouse: new members of the multicopper oxidase protein grouwith differential transcription in liver and brain.";
Biochem. J. 306.505-512(1995).

-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESES AND DERRAPATION OF HYALURONAN WHICH ARE
                                                                                                                                                                                                                                                                                                                                  CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN. IISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2).
                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                             (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                                          (POTENTIAL
                        PROSITE; PS50234; VWFA; 1.
Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
V -> Y (IN REF. 2).
E -> I (IN REF. 2).
W; CA8BF565458E7B2E CRC64;
                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
CHONDROITIN 4-SULFATE,
                                                                                                                                                                                                                                                           (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                           N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 1;
Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        946 AA
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                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                           106580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.1%;
37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
SM00327; VWA; 1.
                                                                                                                                                                                      946
468
1118
263
263
702
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54
702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         946 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                           703
308
118
263
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                                                                         Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITH2_MOUSE
Q61703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                        PROPEP
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                                                                                             SIGNAL
                                                                                                                                            CHAIN
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  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                  BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
 as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 384-865 FROM N.A.
MEDLINE-88066876; PubMed=2446332;
Saller J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.;
"Isolation and characterization of cDNAs encoding the heavy chain of
maman inter-alpha-trypsin inhibitor (I alpha TI): unambiguous
evidence for multipolypeptide chain structure of I alpha TI.";
Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ITH2_HUMAN STANDARD; PRT; 946 AA.
19923; 014659; 015484;
01-PEB-1991 (Rel. 17, created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain H2) (Inter-alpha-inhibitor heavy chain H2) (Inter-alpha-inhibitor heavy chain H2) (Inter-alpha-inhibitor heavy chain H2) (Serum-derived hyaluronan-associated
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88152237; PubMed-2450046; Gebhard W., Schreitmueller T., Hochstrasser K., Wachter E.; "Complementary DNA and derived amino acid sequence of the precursor of one of the three protein components of the inter-alpha-trypsin
                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL). CHONDROITIN 4-SULFATE, CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                    N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
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                                                                                                                                                  Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                 DB 1; Length 946; 0.47;
                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                (BY SIMILARITY). 40DB6716433ED9DC CRC64;
                                                                                                                                                                                                                  SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      5; Mismatches
 non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                212 NVWIIEPQGMRFLHVPDTFEGHFQGVP 23,8
                                                                                                                                                                                                                                                                                                                                                            NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                  Score 60;
                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                              VWFA.
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                                                 EMBL; X70392; CAA49842.1; -. PIR: S54354. S54354. MGD; MGI:96619; ILLO. INTEPPO; IPR005687; VIT. InterPro; IPR005687; VWF_A. PFGN; PR005035; VWF_A. SMART; SM0609; VIT; I. SMART; SM00327; VWA; I.
                                                                                                                                                                                                                                                                                             MW:
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SEQUENCE OF 384-766 FROM N.A.
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37.0%;
                                                                                                                                                                                                                                                                                            946 AA; 105927
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                                                                                                                                        PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                      10; Conservative
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54
702
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468
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55
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                                                                                                                                                             Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein)
                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                             CHAIN
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Pizzo S.V., Hefta S.A.;
Pizzo S.V., Hefta S.A.;
"Presence of the protein-glycosaminoglycan-protein covalent cross-link
in the inter-alpha-inhibitor-related proteinase inhibitor heavy chain
"Ankunin";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malki N., Balduyok M., Maes P., Capon C., Mizon C., Han K.K.,
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon J.;
Tartar A., Fournet B., Mizon C., Hank B., Mizon C., Hank B., Mizon C., Mizon B., Mizon C., Mizon B., Mizon C.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.
MEDLINE-98343966; PubMede-9677337;
Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J.;
"Glycosylation pattern of human inter-alpha-inhibitor heavy chains.";
Blochem. J. 333:749-756(1998).
                                                                                                                                                             "Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning of human inter-alpha-trypsin inhibitor discloses three
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"A serum-derived hyaluronan-associated protein (SHAP) is the heavy chain of the inter alpha trypsin inhibitor.";
J. Biol. Chem. 268:26725-26730(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Posttranslational modifications of human inter-alpha-inhibitor:
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Olsen E.H.N., Rahbek-Nielsen H., Thoegersen I.B., Roepstorff
Enghild J.J.;
                                                               Sesboue R., Bourguignon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English Joycez, Thospersen 1.B., Pizzo S.V., Salvesen G.;
English G.J., Thospersen 1.B., Pizzo S.V., Salvesen G.;
"Analysis of inter-alpha-trypsin inhibitor and a novel try:
inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
Polypeptide chain stoichiometry and assembly by glycan.";
J. Biol. Chem. 264:15975-15981(1989).
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MEDILINE-9323026; Pubmed-7682553;
Enghlid J.J., Salvesen G., Thoegersen I.B., Valnickova Z., Pizzo S.V., Hefta S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. Hoppe-Seyler 368:963-970(1987),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 67-101, AND HYALURONAN BINDING.
                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. Hoppe-Seyler 369:15-18(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 268:8711-8716(1993).
                                                                     Salier J.-P., Diarra-Mehrpour M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94075371; PubMed-7504674;
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MEDLINE=89076497; PubMed=2462430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88024442; PubMed=3663330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         different proteins.
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                                                                                                                       Martin J.P.;
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Best Local Similarity
                                                                                                                          AROG_YEAST
              Matches
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                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    -:- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MARTIX PROTEIN, INCLUDING THOSE ON CELL SURPACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHEISLAND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.

--- SUBBUNIT: L'ALPHA-I PLASMA PROTEASE INHIBETORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HJ, H2 OR H3) AND ONE LIGHT CHAIN, BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) OF H3 AND BIKUNIN, AND PRE-ALPHA-LIKE INHIBITOR (I-ALPHA-L) OF H3 AND BIKUNIN.

--- PTM: HRAVY CHAINS ARE HYBELINKED WITH BIKUNIN VIA A CHONDROITIN CONSTRUCTION OF THE THEIR C-TERMINAL ASPARANTE.

--- SIMILARITY: BELONGS TO THE THEIR FAMILY.

--- SIMILARITY: BELONGS TO THE ITH FAMILY.

--- SIMILARITY: CONTAINS I VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
H2.
identification of glycans and disulfide bridges in heavy chains 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
CHONDROITIN 4-SULFATE, CROSS-LINK SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=CAR_000140.
O-LINKED (GALNAC. . .) (PARTIAL).
/FTId=CAR_000214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease inhibitor; Repeat; Signal; Multigene family; Gamma-carboxyglutamic acid; Glycoprotein.

SIGNAL 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K -> L (IN REF. 5).
P -> A (IN REF. 2 AND 3).
F -> S (IN REF. 2 AND 3).
N -> D (IN REF. 2 AND 3).
V -> A (IN REF. 2 AND 3).
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O-LINKED (GALNAC.)
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O-LINKED (GALNAC. . .).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 146640; -
oc. Go: OGOODOS211; F:plasma glycoprotein; TAS.
InterPro; IPR005587; VII.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWFA.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; X07173; CAA30160.1; ALT_SEQ.
EMBL; M18193; AAA60558.1; -.
EMBL; M33033; AAA59195.1; -.
                         Biochemistry 37:408-416(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              GlycoSuiteDB; P19823; -. Genew; HGNC:6167; ITIH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
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264
651
118
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DB 1; Length 946;

36.6%; Score 53;

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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Submitted (aUG-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: STREEGSPECIFIC CONDENSATION OF PHOSPHOENOLFYRRUVATE (PEP)
AND D-ENTHROSE-4-PHOSPHATE (E44P) GIVING RISE TO 3-DEOXY-D-
ARABINO-EBPTULOSONAET-7-PHOSPHATE (DARF).

-!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
phosphate + H(2)O.

-!- ENZIME REGULATION: INHIBITED BY TYROSINE.
-!- PATHWAX: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
*Cloning, Primary structure and regulation of the ARO4 gene, encoding
the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
synthase from Saccharomyces cerevisiae."
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94078675; PubMed-8256522; Doisgnow F., Biteau N., Aigle M.; Crouzet M.; Meteau N., Aigle M.; Meteomplete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative
                                                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydror-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase); (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
ARO4 OR YBR249C OR YBR1701.
                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales
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-!- INDICTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAMP SYNTHETASE FAMILY.
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                    13;
                                                                                                                                                                                                 370 AA
Pred. No. 5.4;
                    Mismatches
                                                                                212 DVWVIEPQGLRFLHVPDTFEGHFDGVP 238
                                                         1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                   PRT;
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EMBL; L20296; AAA65607.1; -.
EMBL; Z36118; CAA85212.1; -.
33.3%;
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 205-207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 113:67-74(1992).
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SEQUENCE FROM N.A.
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Feldmann K.;
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AP3 OR AT3G54340 OR T12E18_30.
AP3 OR AT3G54340 OR T12E18_30.
AP3 OR AT3G54340 OR T12E18_30.
Babaidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudloctyledons; core eudlocts; Rosidae;
eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                  Gaps
                    SGD; S0000453; ARO4.
GO; GO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .;
InterPro; IPR006219; AroPGH.
InterPro; IPR006218; AAPDI/KDSA.
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STRAIN=cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,
cv. Chl.1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,
cv. Gr-3, cv. Jl-1, cv. Ka-1, cv. Kent, cv. Landsberg erecta,
cv. Li-3, cv. Li-8, and cv Lisse;
MEDLIRE=9912649; PubMed-9927474;
Purugyanan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci: departures
from the equilibrium-neutral model at the APETALA3 and PISTILLATA
genes of Arabidopsis thaliana.";
Genetics 151:839-848(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jack T., Brockman L.L., Meyerowitz E.W.; "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is expressed in petals and stamens."; Cell 68:683-697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
De Simone V., Choisne N., Artiquenave F., Robert C., Brottier P.,
Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-cv. Landsberg erecta;
MEDIINE-95036018; PubMed-7948893;
OKAMOLO H., Yano A., Shiraishi H., Okada K., Shimura Y.;
"Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP3_ARATH STANDARD; PRT; 232 AA.
P35632; 039003; QBLB79; Q987Q3; Q98Q14; Q98Q15; Q98Q16; Q98Q17; Q98Q18, O38Q19; Q98Q1; Q98Q21; Q98Q22; Q98X13; Q1-UUN-1994 (Rel. 29, Created) 01-UN-1994 (Rel. 29, Last sequence update) 15-SPP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                  .;
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                                                                                                    Pfan: PF00733; DAHF_Synth_1; 1.
ProDom: PD005060; AroFGH; 1.
TIGREPAS; TIGR00034, aroFGH; 1.
Aromatic amino acid blosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                      35.9%; Score 52; DB 1; Length 370; 47.6%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                       :| || | | | | |:::||| :|
80 DLEAAQEYALRLKKLSDELKG 100
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STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol. Biol. 26:465-472(1994).
                                                                                                                                                                                                                                                                                                                             1 NLWAAQRYGRELRRMSDEFEG 21
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                             Similarity
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  HSSP; P00886; 1QR7
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Cell 68:6
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Matches
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RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

Rumbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,

Ry Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

Rad Conrad A., Hornischer K., Staver G., Loehnert T.-H., Nordsiek G.,

Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Rad Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Mavarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mawes H.-W.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mawes H.-W.,

RA Monfort A., Malts C., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Rooney T., Rizzo M., Walts A., Otterback T., Fujii C.Y., Shea T.P.,

Creasy T.H., Haas B., Maitt R., Wu D., Pererson J., Van Aken S.,

RA Grass D., Lin X., Nierman W.C., Salzber T., White O., Venter J.C.,

RA Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Riyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Randen C., Wada M., Yasuda M., Tabata S.;

R. Sequence and analysis of chromosome 3 of the plant Arabidopsis

Hallian M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riechmann J.L., Krizek B.A., Meyerowitz B.M.;
Jubmerization specificity of Arabidopsis MaDS Gomain homeotic proteins
APEMALA, APETALAA, PISTILLATA, and AGAMORS.";
Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ng M., ranofsky M.F.; "Activation of the Arabidopsis B class homeotic genes by APETALA1."; Plant cell 13:739-753(2001).
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Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis full length cDNA clones (RAFLs) sequenced by the
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortuum (Salk/Stanford/PGEC).";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-99311297; PubMed-10382288;
MEDLINE-993111297. PubMed-10382288;
Bruel D., Froger N., Pelletler G.;
"Development of amplified consensus genetic markers (ACGM) in lapus from Arabidopsis thaliana sequences of known biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Full-length cDNA from Arabidopsis thallana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 36-128 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    floral organs.";
Nature 409:525-529(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome 42:387-402(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENETIC REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
PubMed=11206550;
Honma T , Goto K ;
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DOMAIN
    VARIANT
                         VARIANT
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                                                                                                                                                                                                                                                                          RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00350; NADS_BOX_1; 1.
PROSITE; PS500066; MADS_BOX_2; 1.
Flowering; Transcription regulation; Activator; Developmental protein; Nuclear protein; DNA-binding; Coiled coil; Polymorphism.
FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILIATA that is required for autoregulation of both AR3 and PI genes. AP3/PI heterodimer interacts with APETALA. or SEPALARA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
                                                                                                                                                                                                                              -i- SUBCELLUIAR LOCATION: Nuclear.
-i- TISSUB SPECIFICITY: Expressed in petals and stamens.
-i- TISSUB SPECIFICITY: Expressed in petals and stamens.
-i- INDUCTION: Positively requilated by the meristem identity proteins APETALAI and LEAFY with the cooperation of UFO.
-i- MISCELLANBONG: Matations in AP3 cause transformation of petals into sepals and stamina into carpels.
-i- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                    \rm SUBUNI\bar{T}_1: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corsacalla-1).
Li-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K -> R (in strain cv. Lisse).
M -> T (in strain cv. Bretagny).
N -> D (in strain cv. Corsacalla
T -> S (in strain cv. Li.8).
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 K-box dimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-BOX.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKANSFAC; TOI//0; -.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D21125; BAA04665.1; -.
AF115798; AAD51887.1; -.
AF115799; AAD51888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF115814; AAD51903.1; -. AL132971; CAB81799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF115800, AAD51889.1;
AF115801, AAD51890.1;
AF115802, AAD51891.1;
AF115803, AAD51892.1;
AF115804, AAD51893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M86357; AAA32740.1; -.
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AY142590; AAN13159.1;
AF056541; AAD41557.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF115807; AAD51896.1;
AF115808; AAD51897.1;
AF115809; AAD51898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF115812; AAD51901.1;
AF115813; AAD51902.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF115810; AAD51899.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY087369; AAM64919.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00432; MADS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
164
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01486; K-box; 1
Pfam; PF00319; SRF-TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A42095; A42095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11746; 1MNM.
TRANSFAC; T01776; -
                                                                                                                                                                                                               form complexes.
                                                                                                                                                   development.
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EMBL;
EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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RA MEDLINE-2228027; Fulded-124/7922;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A lischill S.F., Zeeberge B., Buetow K.H., Schaefer C.F., Bart N.K.,
Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapheton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carnincia P., Prange C. F.
Brownstein M.J., Widnen M.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,
R. Anhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
R. Butterfield Y.S.N., Krzywinski M.L., Skalksk U., Smailus D.E.,
R. Schnerch A., Schein J.E., Jones S.J., M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
R. Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903(2002).
P. SMILARITY: Gontains I Rho-Gap domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                 CV.
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L -> V (in strain cv. Kas-1).
E -> K (in strains cv. Chi-1 and Gr-3).
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                                                                                                                        Length 232;
                                                                                                                                                                                   Indels
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13;
                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   851 AA
                                                                                                                                          Pred. No. 2.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                     107 QRLGECLDELDIQELRRLEDEMENTFK 133
                                                                                                                     Score 51;
Pred. No. 2
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Pred. No.
                                                                                                                                                                                                                                          6 QRYG-----RELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLU-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC031465; AAH31465.1; -.
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                                                                                                                  35.2%;
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Pfam; PF00620; RhoGAP; 1.
SMART; SMQ0324; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50238; RHOGAP; 1.
                                                                                                                     Query Match 35.2
Best Local Similarity 44.4
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein C5orf5 homolog.
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256
   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CE05_MOUSE
Q8K2H3;
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Probably assists in splicing chloroplast group I introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATGRASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                             SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 506;
                                                                                                       "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 VWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LWAA-----QRYGRELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49.5;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01348; Intron_maturas2; 1. 
Pfam; PF01824; MatK_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB012741; BAA25862.1; -.
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36.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA processing; Ch
SEQUENCE 506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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NCBI_TaxID=49629;
    NCBI_TaxID=49622;
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                                                                                                                                                                                                                                     SUBFAMILY
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                            [1]
SEQUENCE I
                                                                                        Yukawa T
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      Gaps
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
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Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%; Score 49.5; DB 1; Length 506; 36.7%; Pred. No. 9; ive 5; Mismatches 7; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
A; 60412 MW; CFEA926307DAC85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Investigation of sectional relationships in the Rhododendron (Ericaceae) based on matk sequences. Shokubutsu Kenkyu Zasshi 73:143-154(1998).
  7;
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Last annotation update)
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Last annotation update)
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5; Mismatches
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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                                           23
                                           2 LWAAQRYGRELRRMSDEFEGSF
                                                                                                                                                                                                                                                                                                                   MATK.
Ledum palustre (Wild rosemary).
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28-FEB-2003 (Rel. 41, Last anno
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15-SEP-2003 (Rel. 42, Last anno
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Best Local Similarity 36.77
Matches 11; Conservative
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  Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-!- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED
FOR THE REPAIR OF OXIDATIVE DNA DAMAGE. CLEAVES THE DNA BACKBONE
BY BETA-DELTA ELIMINATION AS WELL AS 5'DEOXYRIBOSE PHOSPHATE (BY
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-210/4935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhaw G.F., Farns P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Poramousls K.,
Appodaca J., Anantharman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                        7;
                                                                                                         34.1%; Score 49.5; DB 1; Length 506; 36.7%; Pred. No. 9;
                                                                                                                                        Indels
       InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
PRAM; PF0285195; Chloroplast.
SEQUENCE 506 AA, 60569 MW; AEE12FF8809C223E CRC64;
                                                                                                                                      7;
                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endonuclease VIII (EC 3.2...).
NEI OR Z0865 OR ECS0739.
                                                                                                                                                                                               393 VWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                                                                                                                                                                                                                                                                    262 AA
                                                                                                                                      5; Mismatches
                                                                                                                                                                   2 LWAA-----QRYGRELRRMSDEFEGSFK 24
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InterPro; IPR000214; Fapy_DNAglyco_zn.
                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=21156231; PubMed~11258796;
                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae; Escherichia
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE0055249; AAG55037.1; -. EMBL; AP002552; BAB34162.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli 0157:H7.
                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A85572; A85572.
PIR; C90721; C90721.
                                                                                                             Query Match
Best Local Similarity
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END8_ECO57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-35; 188-205 AND 213-226. MEDILINE-9731525; PubMed-9711429; MEDILINE-9731525; PubMed-9711429; Jiang D., Hatahet Z., Blaisdell J.O., Melamede R.J., Wallace S.S.; Escherichia coll endoutlease VIII: cloning, sequencing, and "Escherichia coll endoutlease VIII: cloning, sequencing, and order the nel structural gene and characterization of nei and nel inth mutants."; J. Bacteriol. 179:3773-3782(1997).
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-i- SIMILARITY: BELONGS TO THE FPG FAMILY.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                     DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger;
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of endonuclease III (nth) and endonuclease VIII (nei) mutants of Escherichia coli K-12.";
J. Bacteriol. 179:3783-3785(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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Saito Y., Uraki F., Nakajima S., Asaeda A., Ono K., Kubo K.,
Yamamoto K.;
                                                                                                                                                                                                                                                                           Score 49; DB 1; Length 262; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                        BY SIMILARITY.
POTENTIAL.
37C3C5E236E07A88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
15-701-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endonuclease VIII (EC 3.2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 AA
                                                                                                                                                                                                                                                                                                                                                 Mismatches
Pfam; PF01149; Fapy_DNA_glyco; 1.
ProDom; PD003680; Fapy_DNA_glyco; 1.
PROSITE; PS01242; FPG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPEIRRAADNLEAAIKGKP 21
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29680 MW;
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262 AA;
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es 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN="YZ" / ATCC 700931;
MEDLINE-22531367; PubMed=12644504;
Deng N., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18";
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 185:2330-2337(2003).
-!- FUNTION: IONA N-GLYCOSTARSW WITH AN AP LYASE ACTIVITY. REQUIRED
FOR THE REPAIR OF OXIDATIVE DNA DAMAGE. CLEAVES THE DNA BACKBONE
BY BETA-DELIA ELIMINATION AS WELL AS 5'DECXYRIBGSE PHOSPHATE (BY
                                                                                                                                                                            Prodom; PD003680; Fapy_DNA_glyco; 1.
PROSITE; PS01242; FPG; 1.
DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                        Score 49; DB 1; Length 262;
Pred. No. 5.2;
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                                                                                                                                                                                                                                                              237 260 POTENTIAL.
262 AA; 29714 MW; 5010961768ADC265 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Brdonuclease VIII (EC 3.2.--).
NEI OR STY0771 OR 12148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 AA.
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-!- SIMILARITY: BELONGS TO THE FPG FAMILY.
                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                              PIR; A64807; A64807.

PDB; 1K3W; 04-OCT-02.

BCGGENE; BG13237; no.

InterPro; IPR000191; Fapy_DNA_glyco.

InterPro; IPR000214; Fapy_DNAglyco_zn.

Pfam; PF01149; Fapy_DNA_glyco_zn.

Pfam; PF01149; Fapy_DNA_glyco_zn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                               Complete proteome; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                            9 GRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                         3 GPEIRRAADNLEAAIKGKP 21
             EMBL, U38616; AAC45355.1; -.
EMBL, D89754; BAA20414.1; -.
EMBL, AE000174; AAC73808.1; -.
EMBL; D90710; BAA35378.1; -.
                                                                                                                                                                                                                                                                                                          33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                 EMBL; AE016841; AA069762.1; -
InterPro; PRR000191; Fapy_DNR_glyco.
InterPro; PR0000214; Fapy_DNR_glyco_zn.
Pfam: PF01149; Papy_DNR_glyco; 1.
ProDom; PD00080; Papy_DNR_glyco; 1.
PR0011E; PS01242; PF0;
DNR_repair; Hydrolase; Glycosidase; Endonuclease; Zinc; Zinc-finger;
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6
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POTENTIAL.
4E255C0CCF59A6A3 CRC64;
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262 AA; 29734 MW;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                               Complete proteome.
INIT_MET 0
ZN_FING 237 2
SEQUENCE 262 AA;
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Search completed: September 15, 2003, 17:22:59 Job time : 6.36429 secs

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September 15, 2003, 17:17:31; Search time 29.3143 Seconds (without alignments) 237.680 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                         830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             145
1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                830525 seqs, 258052604 residues
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                                                                             using sw model
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Gapop 10.0 , Gapext 0.5
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sp_fungi:*
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sp_bacteriap:*
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Maximum Match 100%
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sp_mhc:*
sp_organelle:*
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Maximum DB seq length: 200000000
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sp_plant:*
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                                                                             OM protein - protein search,
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Perfect score:
Sequence:
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STIMMARTES

		Description	Q919n2 brachydanio	Q8k016 mus musculu	Q8vjs3 mycobacteri	Q10843 mycobacteri	Q8zy71 pyrobaculum	Q991y6 oryctolagus	Q9seg0 arabidopsis	Q9sq20 arabidopsis	Q9sq22 arabidopsis	Q9sq17 arabidopsis	Q9sq19 arabidopsis	Q9sq21 arabidopsis	Q81b79 arabidopsis	Q9sq16 arabidopsis	Q9sq15 arabidopsis	Q9s7q3 arabidopsis
SOUTHWENTERS		3 ID	13 Q9I9N2	11 Q8K016	16 Q8VJS3	16 Q10843	17 Q8ZY71	6 Q9GLY6		10 Q9SQ20	10 095022	10 098017	10 095019	10 098021	10 Q8LB79	10 09SQ16	10 Q9SQ15	10 098703
		Query Match Length DB	 146	946	196	223	471	946	231	232	232	232	232	232	232	232	232	232
	æ	Query Match	 0.09	41.4	36.6	36.6	35.9	35.9	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2
		Score	 87	09	53	53	52	52	51	51	51	51	51	51	51	51	51	51
		Result No.	 E E	2	m	4	S	9	7	∞	σ	10	11	12	13	14	15	16

51 35.2 232 10 098018 5 34.8 904 2 098033 5 34.8 909 16 088134 5 34.8 990 11 088313 5 34.1 088315 5 34.1 5 55 8 047173 5 34.1 5 66 8 047155 5 34.1 5 66 8 047152 5 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Q9sq18 arabidopsis Q9kgw3 pseudomonas Q8ei34 shewanella Q9c793 arabidopsis Q8x316 mus musculu	Ophnes hallobacteri Q9hnes hallobacteri Q9ssp5 arabidopsis Q8k7h3 mus musculu Q9ub33 anopheles g	18 menziesia 19 rhododendr 11 rhododendr 10 rhododendr	062982 rhododendro 062975 rhododendro 062972 rhododendro 062989 rhododendro 062978 rhododendro 047155 rhododendro		7170 7174 2983
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ALIGNMENTS

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Gaps
                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopteryyli; Neopteryyli; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                           Length 146;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                  zebrafish.";
cell Death Differ. 7:509-510(2000).
EMBL: AR731017; AAF66962.2; -.
HSSP: Q92934 1G57.
ZEIN; ZDB-GEMR-000616-1; bad.
SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                           Query Match 60.0%; Score 87; DB 13; L Best Local Similarity 65.2%; Pred. No. 6.7e-05; Matches 15; Conservative 5; Mismatches 3;
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                      146 AA.
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                                        01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2002 (TrEMBLrel. 22,
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                     PRELIMINARY;
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Q8K016
ID Q8K016
AC Q8K016;
                             0919N2;
                     09I9N2
                                                                       Bad.
RESULT 1
            Q919N2
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MEDLINE—8829587; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Elplaneier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Comor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacteriae, Mycobacteriaceae, Mycobacterium. NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.6%; Score 53; DB 16; Length 223; 58.8%; Pred. No. 11; ive 1; Mismatches 6; Indels
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBER. AE0091936 Aal63125.1; -.
InterPro; IPR00683; Elp3.
InterPro; IPR00683; GCNSacetyltransf.
Pfam; PF00583; Acetyltransf; 1.
SMART; SMO0795 Elp3; 1.
Hypothettcal protein; Complete protecome.
SEQUENCE 471 AA; 52952 MW; 3BIE36E8AEEZEFOA CRC64;
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Pan, PP0231; Transposase_20; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 223 AA; 24132 WW; 70456750017FEF37 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                         08, Last sequence update)
20, Last annotation update)
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EMBL; 274025; CAA98415.1; -.
Tuberculist; Rv2014; -.
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SEGUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubWed=11792869;
                                                               Created)
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   PRT;
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                                                      01-NOV-1998 (TIEMBLED 08, COL.NOV-1998 (TIEMBLED 08, IOL.MAR-2002 (TIEMBLED 20, IHPPCHDED 20, INCLEIN RV2014.
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Matches 10; Conservative
   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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STRAIN-COC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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EMBL; AE007058; AAK46348.1; -.
                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterinae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.6%; Score 53; DB 16; Length 196; 58.8%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.4%; Score 60; DB 11; Length 946; 37.0%; Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034341.1; -.
BMCD; MGI:96619; Itih2.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF.A.
SWART; SW00609; VIT; 1.
PROSITE; PS50234; VWRA; 1.
PROSITE; PS50234; VWRA; 1.
SRART; SW00609; VIT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02371; Transposase_20; 1.
SEQUENCE 196 AA: 21349 MW; C145A8D836FD9C2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2002 (TrEMBIrel. 20, Created)
01-WAR-2002 (TrEMBIrel. 20, Last sequence update)
01-WNV-2002 (TrEMBIrel. 21, Last annotation update)
IS1607, transposase.
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Inter-alpha trypsin inhibitor, heavy chain 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:| : | : | : | 1:|:|
212 NVWIMEPQGMRFLHVPDTFEGHFQGVP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFEGSFKGLP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003346; Transposase_20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bishai W.;
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**08VJS3** 

RESULT 3 Q8VJS3

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                          PRINTS; PRO0404; MADSDOWAIN.
SWART; SM00432; MADS; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
NON_TER 21 231
SEQUENCE 231 AA; 27176 MW; A67CAEIEEEDBF7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Byermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27342 MW; BDFDCB59B73F4601 CRC64;
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                                                                                                                                                                                                                                                                                            Gaps
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STRAIN-cv. Corscalla;
MEDLINE=99126449; PubMed=9927474;
Puruganan M.D., Suddith J.I.;
Puruganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.";
genes of Arabidopsis thaliana.";
genes of Arabidopsis Univarions WCLEAR (BY SIMILARITY).
-:- SUBCELULAR LOCATION: WUCLEAR (BY SIMILARITY).
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                                                                                                                                                                                                                                   Length 231;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                Score 51; DB 10;
Pred. No. 22;
3; Mismatches 4
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Pred. No. 22;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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HSSP, P11746; IMNM.
INTERPRO, IPRO02487; TF, Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00350; MADS_BOX_1; 1. PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01486; K-box; 1.
Pfam; PP00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SWART; SW00432; MADS; 1.
                                                                                                                                                                                                                                      Query Match 35.2%;
Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, Floral homeotic protein AP3.
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Matches 12; Conservative
        Pfam; PF00319; SRF-TF; 1.
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098022;
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDIAL SEQUENCE FROM N.A. Lawton Tauh A.L., Buckler E.S. IV, Puruganan M.D.; Lawton-Rauh A.L., Buckler E.S. IV, Puruganan M.D.; Patterns of molecular evolution among paralogous floral homeotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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0
        DB 17; Length 471;
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                                                                 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB050592; BAB17301.1; Interpro; IPR006587; VIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50234; VWFA; 1.
SEQUENCE 946 AA; 106240 MW; B7AF05434B228CC5 CRC64;
                                                                                                                                                                                                                                                                                                             C9GLV6 PRELIMINAKI; ...., O9GLV6; O9GLV6; O1-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Inter-alpha-trypsin inhibitor heavy chain2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki A.;
"Rabbit inter-alpha-trypsin inhibitor heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 52; DB 6
; Pred. No. 74;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AA.
                                                                 3; Mismatches
                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
        Score 52;
Pred. No.
                                                                                                                                                        1 NLWAAQRYGRELRRMSDEFEGSFKGLP
                                                                                                                       3 WAAQRYGRELRRMSDEFEGSFKGL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Mol. Biol. Evol. 16:1037-1045(1999)
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HSSP, P11746, IMNM.
INTERPRO1, IPR002487, TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam, PF01486, K-box, 1.
        35.9%;
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Interpro; IPR002035; VWF_A.
Pfam; PF00092; vwa; 1.
SMART; SW00609; VIT; 1.
SMART; SM00327; VWA; 1.
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Best Local Similarity 33.34
Conservative
Description
Query Match
Best Local Similarity 41.7'
Matches 10; Conservative
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Q9GLY6
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SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27264 NW; 04FCFC55B73C7729 CRC64;
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DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27311 MW; 71AE593FB8A67EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SETALN-CV. Bretagny;

MEDLINE-991649; PubMed-9927474;

MEDLINE-991649; PubMed-9927474;

Purugganan M.D., Suddith J.I.;

"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana.",

Genetics 151:839-848(1999).

-! SUMILARITY: BELONGS TO THE MADS DOWAIN FAMILY OF TRANSCRIPTION FACTORS.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                               Score 51; DB 10; Length 232; Pred. No. 22;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Floral homeotic protein AP3.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                    232 AA.
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                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                    107 QRLGECLDELDIQELRRLEDEMENTFK 133
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                                                                                                                                                                                                                                                                                                                                    PRT;
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Interpro; IPR002100; TF_MADSbox.
pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF115807; AAD51896.1; -. HSSP; P11746; 1MNM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.2%;
                                                                                                             Query Match 35.2%,
Best Local Similarity 44.4%;
Matches 12; Conservative
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Q9SQ21
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Q9SQ19
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PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27267 MM; 4228520697E22A65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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MNEDLINE-99126449; PubMed-9927474;
Puruganan M.D., Suddith J.L.;
Puruganan M.D., Suddith J.L.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thallana.";
Genetics 151:839-848(1999).
-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-: SUBCELLULAR EDONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Floral homeotic protein AP3.
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                    Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR002100; TF_MADSbox.
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InterPro; IPR002100; TF_MADSbox.
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SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.2%;
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tes 12; Conservative
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Pfam; PF00319; SRF-TF; 1.
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Pfam; PF00319; SRF-TF; 1
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=3702;
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Query Match Best Local S Matches 12

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SMART; SM00432; MADS; 1.
PROSTER; PS00350; MADS_BOX_1; 1.
PROSTER; PS50046; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SEQUENCE 232 AA; 27286 MW; 66976305B8BF63E3 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Floral homeotic protein APPTALA3 (APB).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Subtaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
SUBMCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! - SUBMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                 STRAIN=cv. Kent;
MEDLINE-99126449; PubMed=9927474;
Puruganan M.D., Suddith J.I.;
"Molecular population genetics of floral homeotic loci. Departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidoppis thaliana.";
                                                                                                                                                                                                                                              Genetics 151:839-848(1999).
-!- SUBCELLUTAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 232;
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                              II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 22;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QRYG-----RELRRMSDEFEGSFK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY087369; AAM64919.1; -.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                          EMBL; AF115805, AAD51894.1; -.
HSSP, P11746; 1MNM.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SWART; SW00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.48;
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Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 44.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01486; K-box; 1
Pfam; PF00319; SRF-TF;
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SEQUENCE FROM N.A.
                                                                                            SEQUENCE FROM N.A.
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                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Pfam; PRO1486; K-box; 1.
Pfam; PRO0319; SRF-TE, 1.
PRINTS; PRO0404; MADSDOMAIN.
SMART; SMO0432; MADS; 1.
PROSITE; PS50066; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SROHENCE 232 AA; 27314 MW; DB8CAIFC835557D6 CRC64;
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SEQUENCE 232 AA: 27339 WW; CC90703F959CFAD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                          Length
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Last annotation update)
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Last annotation update)
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22;
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Pred. No. 22;
                                                                                                                                                     Mismatches
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                                                                                                        Score 51;
Pred. No. 2
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                              6 QRYG-----RELRRMSDEFEGSFK 24
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STRAIN-cv. Lisse;
MEDLINE-99126449; PubMed-9927474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF115810; AAD51899.1; -.
HSSP, P11746; IMMM.
InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
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44.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, Floral homeotic protein AP3.
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Best Local Similarity 44.4
Matches 12, Conservative
                                                                                                                                                   Conservative
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                                                                                    Query Match
Best Local Similarity
'.hes 12; Conserve
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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Core curosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;

RN [1]
RN SEQUENCE FROM N.A.

RS STRAIN=CV Kas-1;

RN PRUGGATAN=CV Kas-1;

RN PRUGGATAN=CV Kas-1;

RN PRUGGATAN N.A.

RA MEDLINE-99126449; PubMed=9927474;

RN MEDLINE-99126449; PubMed=9927474;

RN MEDLINE-99126449; PubMed=9927474;

RN PRUGGATAN N.A.

RA MEDLINE-99126449; PubMed=9927474;

RN Genetics 151:839-848(1999).

CC '- SIBCELUTAR LOCATION: NUCLEAR (BY SIMILARITY).

CC '- SIBCELUTAR LOCATION: TE_Kbox.

DR REBL; AFILISB12; AAD51901.1; -.

DR RESP; P11766.1MMM.

DR RESP; P11766.1MMM.

DR RESP; P11766.1MMM.

DR RESP; P11766.1MMM.

DR REMAIN FROMOTO: TE_MADSDOMA.).

DR PÉRM; PROMOTO: TE_MADSDOMA.).

DR PERM; PROMOTO: NADSDOMA.).

DR PERM; PROMOTO: NADSDOMA.).

DR PROSITE; PSO00350; MADS_BOX_1; 1.

DR ROSITE; PSO00350; MADS_BOX_1; 1.

DR ROSITE; PSO0056; MADS_BOX_1; 1.

DR ROSITE; PSO0056; MADS_BOX_2; 1.

ROBER; PROMOTO: TE_MADSDOMA.).

SEQUENCE 232 AA; 27300 MW; 5CA05FD44F824PF0 CRC64;

QUARTY MATCH

DR ROSITE; PSO0056; MADS_BOX_2; 1.

ABACHES 12; CONSECUEDEIDIGERRESDERFECSER 24

III | III | III | III

DD 107 QRVGECLDEIDIGERRESDERFECSER 24

III | III | III | III

DD 107 QRVGECLDEIDIGERREDBENTFR 133
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Search completed: September 15, 2003, 17:25:46 Job time: 30.3143 secs

3

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model
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(without alignments) 112.231 Million cell updates/sec September 15, 2003, 17:16:01; Search time 39.6 Seconds Run on:

US-09-544-664-55 Title: Perfect score:

148 1 KNIWAAQRYGRELRRMSDEFEGSFKGLK/28 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

| SIDESI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
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/SIDSI/gcgdata/genesecq/genesecqprembl/AA1998.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gogdata/geneseg/genesegp-emb1/AA2002.DAT:\*/SIDS1/gogdata/geneseg/genesegp-emb1/AA2003.DAT:\*

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*

### SUMMARIES

Description	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Bcl2 polypeptide B	Shorter murine BAD	bcl-x(L)/bcl-2 ass	Murine BCL-XL/BCL-	Mutant BCL-XL/BCL-
QI		AAB37056	AAB37001	AAB37002	AAB37003	AAB70370	AAR95168	AAW61315	AAW61316
DB	21	21	21	21	21	22	17	13	13
% Query re Match Length DB I	28	27	26	56	27	162	204	204	204
% Query Match	100.0	96.6	93.2	93.2	93.2	93.2	93.2	93.2	93.2
Sco	148	143	138	138	138	138	138	138	138
Result No.	F 25	7	ω ω	5	S	ω	7	80	on

Mutant BCL-XL/BCL-Mutant BCL-XL/BCL-	Murine BAD protein	Longer murine BAD	Murine BAD protein	Bad-DITR apoptosis	Human Bad peptide	PTPC-interacting T	Bcl2 comp	it Bcl2 comp	Bad peptid	Bad be	in for	ol-xL/Bol-	Human cell prolife	BAD	Bad	acio	Human BAD protein	Human ovarian anti	bcl-x(L)/bcl-2 ass	: Bcl2 compe	Human Bad peptide	Mutant Bc12 compet	nt Bcl2 comp	Human Bad peptide	Bad peptid	Human Bad peptide	Bcl2	t Bcl	Bcl	Human Bad peptide	ခွင္ခ	Human Bad peptide	t Bcl	Human Bad peptide
AAW61317 AAW61318	383	9	908	)22	362	ABP56161	348	349	361	362	247	577	351	336	328	768	908	163	516	349	861	348	848	361	861	862	348	349	349	361	361	62	348	AAU78611
19	19	22	24	22	23	23	23	23	23	23	18	13	21	22	22	22	24	23	17	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
204	0	0	0	9	24	25	25	25	25	25	9	168	16	9	9	Q	Q	0	23	25	25	25	25	25	25	23	25	25	25	25	25	25	25	25
93.2	m.	m.	m,	m,	7.	7	7	7.	7.		7.	7	7.	7.	7.	7	Ľ.	۲.	ô.	δ.	5	4	4.	4	4.	ä,	w.	ω.	w.	w.	w.	m	m.	'n.
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10	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; Bcl2 polypeptide BH3 domain peptide #55. AA. AAB37055 standard; peptide; 28 (first entry) 28-FEB-2001 AAB37055; RESULT 1

stroke; myocardial infarction 99US-0128202. 06-APR-2000; 2000WO-US09352 WO200059526-A1. Homo sapiens. 12-OCT-2000. AND SERVICE SE

Lu Z; Wang J, Zhang Z, Shan S, (UYJE-) UNIV JEFFERSON THOMAS. Huang Z,

07-APR-1999;

WPI; 2000-679325/66

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain in northonal group is or COMH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or COMH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or conventioned with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides Aba37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/laukemia 2 (BC1-2) mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting BC1-2 cunction. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express BC1-2. The cancer includes prostate, colorectal, gastric, conspused is also useful for treating a subject and non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for treating disorders characterized by concer cells that conjugate is anonytes a conjugate is also useful for treating disorders characterized by increased anonytes or members a group of the conjugate is a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bol-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma, melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
              New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 148; DB 21;
100.0%; Pred. No. 1.4e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcl2 polypeptide BH3 domain peptide #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB37056 standard; peptide; 27 AA
                                                                                                               Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stroke; myocardial infarction.
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Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AA;
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The invention relates to a peptide conjugate having the formula:

(R.X)n peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where to the N-terminus of the peptide where to the N-terminus of the peptide where the functional group of the side chain is NHZ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is COCH or CONHZ; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-B3708 represent examples to phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides corresponding to amino acids 72-97 of the peptide portion of the conjugate. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2), mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflited with a cancer characterized by cancer collinger or cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer characterized by cancer conjugate is also useful for treating disorders, acquired conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                      New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                                                                   Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stroke; myocardial infarction.
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  Huang Z, Wang J, Zhang Z,
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Best Local Similarity 100.
Matches 27; Conservative
                                             WPI; 2000-679325/66.
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Zhang Z, Shan S,

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                                                                                                                                                                                                                                                     2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                 Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                            AAB37002 standard; peptide; 26 AA.
                                                            Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                    stroke; myocardial infarction
    (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                  28-FEB-2001 (first entry)
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                           WPI; 2000-679325/66.
                                                                                                                                                                                                                    26 AA;
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                 Huang Z,
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Matches
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ID AAB
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Bcl-2. The cancer includes prostate, colorectal,

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = 0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain in NH2 or OH; or X = 0 or NH, or CONH2; and R = 2-18C alkyl or alexy, 2-14C alkylenyl containing one or convent; and R = 2-18C alkyl or alexy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides Abaly1001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphomal-leukemla 2 (BC1-2)-mediated blockage of reversing B cell lymphomal-leukemla 2 (BC1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting BC1-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer celased by cancer cells that contains and subject afflicted with a cancer celased by cancer cells that
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                                                                                                                                                                                                                                                                                                                                                      New peptide conjugates for modulating apoptosis or for inhibiting B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                          (UYJE-) UNIV JEFFERSON THOMAS
06-APR-2000; 2000WO-US09352.
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                                                                                                                                                                                                               Huang Z, Wang J,
                                                                     07-APR-1999;
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       The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the Netherland of the peptide where to the N-terminus of the peptide, or a side chain of the peptide where the functional group is attached to the C-terminus of the peptide, or a side chain is NH2 or OH; or X = 0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is COOH or COOH of the peptide, where the side chain functional group is COOH or COOH of the peptide alkoxy, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides A-B37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of goptosis in cancer cells of a subject of inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for inhibiting a cubject afflicted with a cancer characterized by cancer cells that cancer characterized by cancer cells that chancer includes prostate, colorectal, gastric, or consensal lung, remain or thyroid cancers, neuroblemia, or
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hes 0;
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Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bol-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung, remal; thyroid; neuroblastoma;
                                                                                                                                                                                                                                                          melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
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0; Gaps Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bol-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma, melanoma; lymphocytic\_leukemia; neurodegenerative disorder; AIDS; . 0 93.2%; Score 138; DB 21; Length 26; 100.0%; Pred. No. 4.6e-14; Indels 100.0%; Prec. .... Bcl2 polypeptide BH3 domain peptide #3. 27 2 NLWAAQRYGRELRRMSDEFEGSFKGL AAB37003 standard; peptide; 27 AA. stroke; myocardial infarction. (first entry) 26; Conservative Similarity 26 AA; WO200059526-A1 Homo sapiens. 28-FEB-2001 Sequence AAB37003; Query Match Local Best Loca Matches RESULT 5 AAB37003 ð g

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(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O OH NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkylenyl of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkylenyl optionally monsubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AB37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides colds 72-97 of the BH3 domain of the conjugate. The peptide conjugate is useful for modulating apolyosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of represent else, it is also useful for inhibiting actoring subject afflicted with a cancer characterized by cancer cells, that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             express Bc1-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                      New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
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                                                                                                                                                                                               Huang Z, Wang J, Zhang Z, Shan S,
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                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 17; 74pp; English.
                                                                                                                                                   (UYJE-) UNIV JEFFERSON THOMAS.
                                                               06-APR-2000; 2000WO-US09352.
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                  12-0CT-2000
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The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amino acid sequence of a mutant Call XIAD-12 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Sarl18 of a human BAD, Ser155 of a murine BAD, (longer murine BAD) or Ser113 of a murine BAD (softer murine BAD) or Ser13 of a murine BAD, contropic, antischaemic, vulnerary, cytostatic, antiviral, neuroprotective, notizopic, antischaemic, vulnerary, cytostatic, antiviral, can be used as an apoptosis inducer or inhibitor. BAD polypeptides and colyncleotides can be used for screening candidate compounds and contropic or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inmunodeficlency diseases, neurodegenerative diseases, ischaemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and cautoimmune diseases. The present sequence represents a specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Pred. No. 3.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 148-149; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                 (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                               99US-0136783.
                                                                                                                                                                                                                                      30-MAY-2000; 2000WO-US11864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-138734/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AA;
                                                                                                  WO200110888-A1.
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Mus musculus.
Synthetic.
                                                                                                                                                                                                                                                                                                               28-MAY-1999;
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                                                                                                                                                                        15-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR95168;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou X;
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ŏ 원 WO9613614-A1

Domain Domain

Region Region

09-MAY-1996.

31-0CT-1995; 31-OCT-1994;

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 504 as asquence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (1) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral inflammation and autoimmune disease. Polynucleotide sequences encoding inflammation and autoimmune disease. Polynucleotide sequences encoding transgenic animals for use as disease models or in drug screening. BAD proteins can be used a specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as ALDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is certained by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated BAD, by usual immunoassays. Mutant BAD which can become phosphated on the specified Ser, forming a product that does not content of phosphorylated on the specified Ser, forming a product that does not content of proteins in the cytosol, thus promoting cell survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                   New mutant BAD polypeptide with phosphorylatable serine replaced -useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4.5e-13; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant BCL-XL/BCL-2 associated cell death regulator #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 10; 95pp; English.
                                                                                                   97WO-US19175.
                                                                                                                                                   96US-0733505.
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Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                    WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 AA;
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV27833
                                                                                                                                                                                                                                                       Korsmeyer SJ;
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WO9817682-A1.
                                                                                                   17-0CT-1997;
                                                                                                                                                   18-OCT-1996;
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Synthetic.
                                                 30-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kp protein which interacts with cl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BHI and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid seasys and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), and its also counters the accelerate apoptoric cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L), and its also counters the cell normal and propressing bcl-x(L). Bad competes with Bax for binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 138; DB 17; Length 204; 100.0%; Pred. No. 4.5e-13;
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                                                 /note= "BH1 conserved amino acids"
                                                                                                   /note= "BH2 conserved amino acids"
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26; Conservative 0; Mismatches
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                                                                                                                                                                                                       /note= "PEST sequence"
                                                                                                                                                /note= "PEST sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. AIDS, senescence or ischaemia.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW61315 standard; Protein; 204 AA.
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                                                                                                                                                                                                                                                                                                                                                        95WO-US14246.
                                                                                                                                                                                                                                                                                                                                                                                                        94US-0333565.
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                                                                            191..192
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                                                                                                                           38..61
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Best Local Similarity
Matches 26; Conserva
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N-PSDB; AAT29479.
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Gaps

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AAW61315;

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Sequence

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Korsmeyer SJ;

17-OCT-1997; 18-OCT-1996;

30-APR-1998.

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The present invention describes mutant BAD (BCL-XI/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the mutant BAD 914 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, Imphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polymotelectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated as sequences. Inhibitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, altoritated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated bAD, by usual immunoassays. Mutant BAD proteins have phosphorylated on the specified Ser, forming a product that does not neterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family serimined by measuring relative amounts of phosphorylated or neterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family serimined by activity thus will survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-XL/BCL-2 associated cell death regulator; BAD protein;
                                                                                                                                                                                                                                                                                                                       New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine substituted mutant; apoptosis; cancer; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 138; DB 19; 100.0%; Pred. No. 4.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 60; 95pp; English.
                                            97WO-US19175.
                                                                                             96US-0733505.
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Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                 WPI; 1998-261422/23.
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                                                                                                                                                                                                                                                                                                                                                                      viral infection
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                                            17-0CT-1997;
                                                                                                                                                                                                Korsmeyer SJ;
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                                                                                             18-OCT-1996;
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30-APR-1998
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Synthetic.
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d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/cur 136, relative to the murine BAD 904 as sequence. The position 112 and/cur 136, relative to the murine BAD 904 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that channesses intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease. Polynucleotide sequences encoding intable animals for use as disease. Polynucleotide sequences condinibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated and the specified Ser, forming a product that does not phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-XL but instead binds to 14-3-3 family ser substituted cannot bind 14-3-3.
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                                                                                                                                                                                                                                                                                                                                            New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 138; DB 19; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW61317 standard; Protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 59; 95pp; English.
                                                                                                                    96US-0733505.
                                                                   97WO-US19175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                   (UNIW ) UNIV WASHINGTON.
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Best Local Similarity 1
                                                                                                                                                                                                                                                                   WPI; 1998-261422/23.
N-PSDB; AAV27834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA;
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Sequence

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Gaps

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07-0CT-1998

AAW61317;

RESULT 10 AAW61317

δÃ 셤 WO9817682-A1

Synthetic.

Mus sp

Length 204; Indels

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This sequence represents a novel serine-phosphorylated protein, BAD (BC1-X1/Rc1-2 associated cell death requiator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction requiator.

Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, senescence, neurodegenerative disease, ischemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, infammation and autoimmune diseases. Messuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulant; neuroprotective; nootropic; antiischaemic; vuleerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; arthritis; infection; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                       Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%; Score 138; DB 19; 100.0%; Pred. No. 4.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB70369 standard; protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 8; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000WO-US11864
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                                                                       97WO-US15871
                                                                                                                         96US-0707868.
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                                                                                                                                                                           (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                             WPI; 1998-207049/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200110888-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-1999;
                                                                                                                                                                                                                           Korsmeyer SJ;
                                                                       09-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2001
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                     12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB70369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (1) fragion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polymuciectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transpenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Wutant BAD proteins have phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4.5e-13; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 60-61; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW58832 standard; protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation; autoimmune diseases
                     97WO-US19175.
                                                                       96US-0733505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
                                                                                                                            (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                             WPI; 1998-261422/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine BAD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA;
                                                                                                                                                                                                                                                     N-PSDB; AAV27836
                                                                                                                                                                                                                                                                                                                                                         viral infection
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                     17-OCT-1997;
                                                                                                                                                                              Korsmeyer SJ;
                                                                       18-OCT-1996;
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Seguence

Query Match

Matches

δŏ g AAW58832;

AAW58832

Mus sp.

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Gaps

0

Indels

Length 204;

Zhou X;

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The present invention describes a method (M1) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids of a Id8 residue amino acids sequence (see ABR39081), where the peptide comprises seril2, seril35, or seri55, or their combinations. BAD has virucide activity. M1 is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 is useful for treating a patient infected with HSV. The present sequence represents murine BAD, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                         Inducing apoptosis in a cell infected with herpes simplex virus, HSV, by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 138; DB 24;
Pred. No. 4.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bad-DTTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 NIWAAORYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
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Corynebacterium diptheriae.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NLWAAQRYGRELRRMSDEFEGSFKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU00220 standard; Protein; 567 AA.
                                                                                                                                        Claim 15; Page 168; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Youle RJ, Liu X, Collier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2000; 2000WO-US22293
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nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-218343/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS00248.
N-PSDB; ABZ81201.
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Chimeric - C
Chimeric - S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated or synthetic polypeptide

(1) comprising a less than full length amino acid sequence of a mutant

BL-XL/BOL-2 associated cell death regularor polypeptide (BAD) or its
fragment, which contains amino acid substitutions at Seril3 of a human

BAD, Seri55 of a murine BAD (longer murine BAD) or Seril3 of a murine

BAD (shorter murine BAD). (1) has immnostimulari, neuroprotective,
nootropic, antilnflammatory and immunosuppressive activities, and
antiarthritic, antilnflammatory and immunosuppressive activities, and
con be used as an apoptosis inducer or inhibitor. BAD polyapetides and
polynucleotides can be used for screening candidate compounds and drugs
for activity that promote cell survival or apoptosis. Other uses include
inducing or inhibiting apoptosis in a cell. Candidate compounds
inducing or inhibiting apoptosis in a cell. Candidate compounds
inducing or inhibiting apoptosis are useful in treating
immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
death, reperfusion cell death, wound healing, cancer, viral infections,
lymphoproliferative conditions, arthritis, infertility, inflammation and
autoimmune diseases. The present sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                         New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 204;
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nes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%; Score 138; DB 22;
100.0%; Pred, No. 4.5e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NEWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR39082 standard; Protein; 204 AA.
                                                                                                                                                                                                                                                                            Claim 4; Page 148; 157pp; English.
                        (APOP-) APOPTOSIS TECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine BAD protein SEQ ID NO:4.
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Best Local Similarity 100.0
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCH-) UNIV CHICAGO
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                                                                                                                WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA;
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Sequence

ABR39082;

RESULT 14 ABR39082

δŽ 셤

0;

Gaps . 0

Length 204; Indels

Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell

Claim 4; Page 59-61; 65pp; English

The sequence represents the amino acid sequence of Bad-DTTR apoptosismodifying fusion protein comprising Bad gene sequence fused via a short individual apoptosis-modifying fusion protein is capable of binding a functional apoptosis-modifying fusion protein is capable of binding a target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein comprises at least two domains: the DTR domain, which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying target cell. The fusion protein is useful for modifying of the target cell. The fusion protein is useful for modifying to finbiting or enhancing) apoptosis in a target cell, such as neuron, improvate, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischemic neuronal injury.

Completion of any conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer sa disease, Huntington's disease, spinal muscular arcophy, stroke episodes and unrequiated cell growth as in tumours and various cancers. The apoptosis-modifying fusion protein can be delivered of effectively throughout the body and targeted to selective tissue and 

567 AA; Sequence

ö Gaps 0; 93.2%; Score 138; DB 22; Length 567; 100.0%; Pred. No. 1.4e-12; Live 0; Mismatches 0; Indels ( 26; Conservative Best\_Local Similarity Matches 26; Conserv Query Match

2 NLWAAQRYGRELRRMSDEFEGSFKGL 27

ΩŽ g

161 NLWAAQRYGRELRRMSDEFEGSFKGL 186

Search completed: September 15, 2003, 17:22:14 Job time: 39.6 secs

Sequence 744%,
Sequence 27, Appl
Sequence 27, Appl
Sequence 21, Appl

20, Appl 18729, A

Sequence Sequence S

Sequence

Sequence 1, Appli Sequence 31658, A Sequence 5180, A Sequence 2, Appli Sequence 4, Appli Sequence 17508, A Sequence 28775, A Sequence 28775, A

4656, Ap 19594, A 3, Appli 3, Appli 1, Appli 31458, A 23807, A

Sequence Sequence

OM protein

Run on:

Sequence:

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93.2%; Score 138; DB 1; Length 204;
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APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: Bcd-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STRIE: California
COMMER: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Deduced amino acid sequence of mouse BAD."
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COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-0CT-1994
CLASSITECATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000700
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELEPHONE: (415) 326-4422
INPORMATION FOR SEQ ID NO: 2:
US-09-328-352-4656
US-09-52-91A-19594
US-09-52-91A-19594
US-09-38-774-3
US-09-252-991A-31458
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US-09-252-991A-1508
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US-09-252-991A-1508
US-09-552-91A-28775
US-09-650-650-650-6775
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US-09-206-551-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 26; Conservative
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LOCATION: 1..204
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81.144 Million cell updates/sec
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Sequence 2, Ay
Sequence 10,
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Sequence 55,
Sequence 56,
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Sequence 40,
                                                                                                                                                                                                                            September 15, 2003, 17:22:21; Search time 14.6 Seconds
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Sequence 2
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Sequence 7
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                             148
1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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RESULT 4

US-08-733-505A-12

Sequence 12, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SELL-XL/BCL-2 ASSOCIATED DUTANTS OF

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAFERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 138; DB 2; I
100.0%; Pred. No. 1.5e-13;
ive 0; Mismatches 0;
ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 PCRSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 NLWAAORYGRELRRMSDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION UNMERR: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6188
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 96
TELECOMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 204 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.2
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-733-505A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                           COUNTRY:
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APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BELLAL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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of mouse BAD."
                                                                                                                                                                                                                          APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
CORRESPECT TOWNSEND and Townsend Mourie and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/661,479
FILING DATE: 11.7UN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-0UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRICATION NUMBER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,233
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
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  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08733505A
Patent No. 5856445
                                                                                                                                 US-08-661-479-2
; Sequence 2, Application US/08661479
; Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: CUS-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                           STREET: 379 Lytton
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KORSMET
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US-08-733-505A-1
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BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR 60
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APPLICANT: Horne, William A.

ATTLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic TITLE OF INVENTION: Acids and Methods of Use

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 138; DB 2; Length 204; 100.0%; Pred. No. 1.5e-13; Live 0; Mismatches 0; Indels
  SERINE SUBSTITUTED MUTANTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NOMBER: 0S/08/717,123 FILING DATE: 20.5EP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                  ADDRESSEE: HOWELL & HAPERKAMP, L.C.
STRERT: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
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                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 965458
TELECOMOUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08717123 Patent No. 5965703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4370 La Jolla Vi
CITY: San Diego
STATE: California
COUNTRY: United States
21P: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 204 amino acids TYPE: amino acid STRANDEDNESS:
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Best Local Similarity 100.
Matches 26, Conservative
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MOLECULE TYPE: peptide
TITLE OF INVENTION: SEI
TITLE OF INVENTION: BCI
NUMBER OF SEQUENCES: 6(
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                        COUNTRY:
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TITLE OF INVENTION: SERINE SUBSTITUTED MOTANTS OF
TITLE OF INVENTION: BCL.XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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Pred. No. 1.5e-13;
                                                                                                                                                                    Length 204;
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                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                      Score 138; DB 2; I
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                    Query Match 93.2%; Score 138; DE Best Local Similarity 100.0%; Pred. No. 1.5 Matches 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                             2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/ACRET INFORMATION:

ATTORNEY/ACRET INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 965458

TELEPHONE: (314) 727-5188

TELEPHONE: (314) 727-5188

INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08733505A; Patent No. 5856445; Garberal INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 204 amino acids amino acid
                      : 204 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 26; Conservative
SEQUENCE CHARACTERISTICS
                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 63105
                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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US-08-733-505A-14
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                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
APPLICANT: Oltersdorf, Tilman
TILE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TILE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.0%; Score 114; DB 2; Length 168; 91.7%; Pred. No. 5.5e-10; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB 1;
Pred. No. 5.4e-10;
0; Mismatches 2
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CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NLWAAQRYGRELRRMSDEFEGSFK 25
                   NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMUNICATION INFORMATION:
TELEPAX: (352) 375-8100
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08717123
Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 77.0%;
Best Local Similarity 91.7%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 168 amino acids
amino acid
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Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-717-123-2
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APPLICANT: Horne, William A.
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140.42801
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                   Score 135; DB 2; Length 204;
Pred. No. 4.2e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135; DB 4; Length 204;
Pred. No. 4.2e-13;
1; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: RIDAPY disk

COMPUTER: IBM FC compatible

COMPUTER: DATE FC FC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERAT
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REFERENCE/DOCKET NUMBER: P-ID 1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09375257 Patent No. 6504022
                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPA: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                      91.2%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%;
96.2%;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.28
Matches 25, Conservative
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Matches 25; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Mus musculus
US-09-375-257-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-717-123-3
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US-08-665-617-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
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77.0%; Score 114; DB 3; Length 168. 91.7%; Pred. No. 5.5e-10; tive 0; Mismatches 2; Indels
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Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettle
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: FILEd Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: Facterog for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
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3174 Porter Dr.
                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0421 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7%
.....has 22; Conservative
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank
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CITY: Palo Alto
STATE: CA
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LIBRARY: General Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of 
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                                                                                                                                                                                        94304
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                                                                                                                                  CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CLONE: 1
US-08-985-335-7
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                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                        GENERAL INCORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Hilman, Jennifer L.
APPLICANT: Tao, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: 9F-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-055
TELEPHONE: 650-845-0466
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 NLWAAQRYGRELRRMSDEFVDSFK 126
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Patent No. 6080847
GENERAL INFORMATION:
                                                                                                                            Sequence 1, Application US/08985335 Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.0%;
Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1
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STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-985-335-7
                                                                      RESULT 11
US-08-985-335-1
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RESULT 15
US-09-375-25-2
; Sequence 2, Application US/09375257
; Patent No. 6504022
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.,
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HOMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; TILE REPERRENCE: 480140/42801
; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                  77.0%; Score 114; DB 3; Length 168; 91.7%; Pred. No. 5.5e-10; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.0%; Score 114; DB 4; Length 168; 91.7%; Pred. No. 5.5e-10; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 15, 2003, 17:45:06 Job time : 14.6 secs
                                                                                                                                                                                                                                                                  103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFK 25
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Best Local Similarity 91.7°
Matches 22; Conservative
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-375-257-2
                  TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
                                                                                                                                                                      Best Local Similarity Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE.
SEQ ID NO 2
                                                                                                      US-09-410-372-7
                                                                                                                                                    Query Match
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Query Match

Dest Local Similarity 91.7%; Pred. No. 5.5e-10;

Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09410372

Sequence 7, Application US/09410372

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tue, Heary
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTIFERATION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: UGA
LIP: 94304
COMPUTER READABLE FORM:
MODIUM TYPE: Diskette
COMPUTER: IBM Compatible
ONFUTER: IBM Compatible
OFFWARE: Fastes for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 9F-0421 US
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPANCE/DOCKET NUMBER: PF-0421 US
TELEPANCE/OFOCKET NUMBER: PF-0421 US
TELEPANCE GO-855-0555
TELEPANCE GO-855-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGHT: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIMBERAY: SYNORABOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:
PRIOR APPLICATION NUMBER: 05/09/410,3/2
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
RAME: BILLINGS, LAUGY J.
REGISTRATION NUMBER: PF-0421 US
TELEPHONE: 650-845-055
TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 NEWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
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US-09-410-372-7
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(without alignments)
184.034 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US07_NWW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_NWP_PUB.pep:*

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3. (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4. (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3. (cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4. (cgn2_6/ptodata/1/pubpaa/US10A_
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/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-544-664-55
148
1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                    using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                    - protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3, Appli Sequence 258, Appli Sequence 258, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 147, Appli Sequence 147, Appli Sequence 1077, Appli Sequence 241, Appli Sequence 241, Appli Sequence 3, Appli Sequence 3, Appli Sequence 162, App Sequence 11541, A Description 1 US.10-066-179-3 US-10-059-261-258 US-09-922-378-2 US-09-894-657-1 US-09-894-657-1 US-09-894-657-7 US-10-066-179-2 US-10-174-1058-147 US-10-128-761-19145 US-10-092-750-1 US-10-092-750-1 US-10-092-750-1 US-10-092-750-1 US-10-092-750-1 US-10-156-761-11541 US-09-922-378-3 SUMMARIES 11 Match Length DB 77.0 777.0 777.0 777.0 777.0 33.1 33.1 29.7 29.7 Query Score Result 8

Sequence 5704, Ap Sequence 12463, A Sequence 12, Appli Sequence 2, Appli Sequence 395. Appli Sequence 395. Appli Sequence 18, Appli Sequence 2, Appli Sequence 1348, Appli Sequence 1348, Appli Sequence 1348, Appli Sequence 1348, Appli Sequence 501, Appli Sequence 5	6 501, 8 292,
US-09-815-2 US-10-008- US-10-008- US-10-369- US-09-864-7 US-09-864-7 US-09-864-7 US-09-864-7 US-09-813-8 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-09-149-0 US-10-156-0 US-10-156-0 US-10-156-0 US-10-156-0 US-09-989-7 US-09-989-7 US-09-989-7	US-09-989-731 US-09-989-732 US-09-991-073 US-09-990-320 US-09-990-444
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                                                                          GENERAL INCORDICATION AND APPLICANT: HOTHER, William A. APPLICANT: OlderGoof, Tilman A. APPLICANT: OlderGoof, Tilman TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE FILE REPREBENCE: 480140.428033 CURRENT APPLICATION NUMBER: US/09/922,378 CURRENT PILING DATE: 2001-08-03 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      %30-10-066-179-3
) Sequence 3, Application US/10066179
) Publication No. US20020115631A1
) GENERAL INFORMATION:
) APPLICANT: HOTNE, William A.
) APPLICANT: OltersADOrf, Tilmen
) TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
) TITLE OF INVENTION: ACIDS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                     91.2%; Score 135; DB 9; Length 204; 96.2%; Pred. No. 8.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
                                      Sequence 3, Application US/09922378 Patent No. US20020037869A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Conservative
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             204
RESULT 1
US-09-922-378-3
                                                                                                                                                                                                                                                                                                                                                                                            US-09-922-378-3
                                                                                                                                                                                                                                                                                                                           LENGTH: 204
TYPE: PRT
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                                                                  Length 168;
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                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastENG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Un-2001
PROPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.0%; Score 114; DB 9; L
91.7%; Pred. No. 7.2e-09;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                               Score 114; DB 9;
Pred. No. 7.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REPERBNCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-894-657-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 NLWAAQRYGRELRRMSDEFVDSFK 126
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                                                                                                                                                   2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09894657; Patent No. US20020098569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                               77.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: SYNORAB01
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      Yue, Henry
Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 91.7 Matches 22; Conservative
                                                                                                         22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
COUNTRY: USA
  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                               Query Match
Best Local Similarity
Matches 22; Conserv
                        US-09-922-378-2
                                                                                                                                                                                                                                                           RESULT 5
US-09-894-657-1
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US-09-894-657-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 258, Application US/10059261
; Sequence 258, Application US/20030077826A1
; Senter Edel No. US20030077826A1
; SENERL INFORMATION:
; APPLICANT: BELMAN, LENA
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: GHANETC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PIPC)
; TITLE OF INVENTION: (PIPC)
; TITLE OF INVENTION: (PIPC)
; TITLE OF INVENTION: (PAPC)
; FILE REPERENCE: 03495, 0216
; CURRENT FILING DATE: 2002-08-29
; PRIOR RELING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: patentin Ver: 2.1
; SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09922378
Patent No. US20020037869A1
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HOMAN BAD POLYBEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HOMAN BAD POLYBEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 201-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                   91.2%; Score 135; DB 14; Length 204; 96.2%; Pred. No. 8.2e-12; live 1; Mismatches 0; Indels
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             CURRENT APPLICATION UNMER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
LENGTH: 204
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                            140 NLWAAQRYGRELRRWTDEFEGSFKGL 165
                                                                                                                                                                                                                                                                                                                    2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown Organism
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.2
Matches 25; Conservative
                                                                                                                                                                   ; ORGANISM: Mus musculus
US-10-066-179-3
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US-09-922-378-2
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TYPE: PRT
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1.0CAFION: (8)..(8)
5.CTATION: (9)..(8)
7.CTATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
0S-10-174-105A-147
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                                                                       Ouery Match 77.0%; Score 114; DB 14; Length 168; Best Local Similarity 91.7%; Pred. No. 7.2e-09; Matches 22; Conservative 0; Mismatches 2; Indels (
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Pred. No. 0.00097;
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100.0%; Pred. No. v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                103 NLWAAQRYGRELRRMSDEFVDSFK 126
                                                                                                                                                         2 NLWAAQRYGRELRRMSDEFEGSFK 25
                                                                                                                                                                                                                                                                          US-10-174-105A-147; Sequence 147, Application US/10174105A; Publication No. US20030068652A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHIBA, FADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HTTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GRELRRMSDEFEGS 23
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Best Local Similarity 100.
Matches 14; Conservative
                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-156-761-9145
                                       US-10-066-179-2
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; Publication No. US20020115631A1
; Publication No. US20020115631A1
; GENERAL INFORMATION:
; APPLICANT: HOLOR, William A.
; APPLICANT: OlterSoforf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REPRENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 2.
; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.0%; Score 114; DB 9; Length 168; 91.7%; Pred. No. 7.2e-09; tive 0; Mismatches 2; Indels
                                                                                                                                                         TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
RAPPLICATION NAMER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF-0421 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATPLICATION NUMBER: 09/410,372
ATPLICATION NUMBER: 09/410,372
ATTORNEY AGREY INFORMATION:
NAME: Billings, incy J.
REGISTRATION NUMBER: 36,749
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Sequence 7, Application US/09894657
Patent No. US20020098569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                    Preeti
                                                                                                                       Shah, Purvi
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                                                                                  Yue, Henry
                                                                                                                                                                                                     NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                 CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alpin, Julia-
APPLICANT: Alpin, Julia-
APPLICANT: Mright, Martin C.
ITLE OF INVENTIVE Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US,10/092,750
CURRENT APPLICATION NUMBER: US,0774,526
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR APPLICATION NUMBER: US 60/274,526
SPRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 241
LENGTH: 138
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TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
INHIBITOR HEAVY CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
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REFERENCE/STOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-655-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <unstraint of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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86 IWIAQ----ELRRIGDEFNAYY 103
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                                                                                                                                                                      RESULT 12
US-10-092-750-241
Sequence 241, Application US/10092750
Sublication No. 0520030032157A1
GENERAL INFORMATION:
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          3 LWAAQRYGRELRRMSDEFEGSF 24
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hammond, Philip W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-092-750-241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1077, Application US/10238075
Sequence 1077, Application US/2030148324A1
GENERAL INFORMATION:
APPLICANT: I.N.S.B.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of their PILE REPERENCE: BLANDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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Pred. No. 37;
                                                                                                                                                                                                                                                                        Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.8%; Score 47; DB 15; Length 35; 45.5%; Pred. No. 6.7; tive 3; Mismatches 5; Indels
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APPLICANT: Wright, Martin C.
TITLE OF INVENTION: POLYPEPTIGES Interactive with BCL-XI
FILE REFERENCE: 50036/050000
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION WUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFUTWARE: Patentin version 3.1
LENGTH: 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FRASEEG for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35
                                                                                                                                                                                                                                                                        Score 52;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                               :|:| :|||| || :|
108 ERWGGDLRRMRDEADGKVPELR 129
                                                                                                                                                                                                                                                                                                                                                                                                        7 ORYGRELRRMSDEFEGSFKGLK 28
                                                                                                                                       ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9145
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40.7%;
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45.5%;
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.55
Matches 10; Conservative
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Matches 10; Conservative
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US-10-238-075-1077
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Matches 11; Conservative
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CRGANISM: Homo sapiens

US-10-092-750-1
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US-10-238-075-1077
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US-10-092-750-1
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Score 44; DB 15; Length 272;
Pred. No. 1.5e+02;
2; Mismatches 5; Indels
                                       APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKALI, YOSHITUKI
APPLICANT: HATTORI, MASHHRA
TITLE OF INVENTION: NOVEL POLYNCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PLING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11541
ILENGTH: 272
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Streptomyces avermitilis US-10-156-761-11541
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                        HORIKAWA, HIROSHI
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Best Local Similarity 53.33
Matches 8; Conservative
ISHIKAWA, JUN
                        APPLICANT:
APPLICANT:
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Pred. No. 1.5e+02;
4; Mismatches 8; Indels
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Best Local Similarity 30.8%; Pred. No. 2.7e+02;
Matches 8; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reddie, James
APPLICANT: Filgrim, Marsha
APPLICANT: Filgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Rechman, Jose Luis
APPLICANT: Vu, Guo-Liang
APPLICANT: Vu, Guo-Liang
APPLICANT: Pineda, Omalra
IILE REFERENCE: MBL-0025
CURRENT APPLICATION NUMBER: US/09/934,455
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIDRARY: GENEBANK
CLONE: gi33985
SEQUENCE DESCRIPTION: SEQ ID NO: 3;
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US-10-156-761-11541
Sequence 11541, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001.08.22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR PILING DATE: 2000.08.22
PRIOR PLICATION NUMBER: MBI-00.2
PRIOR RPLICATION NUMBER: MBI-00.2
PRIOR PILING DATE: 2001.11.16
PRIOR RPLILNG DATE: 2001.04.17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 162
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 162, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
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CRGANISM: Arabidopsis thaliana
US-09-934-455-162
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Best Local Similarity 40.7%;
Matches 11; Conservative 4
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APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
                          INFORMATION FOR SEQ ID NO: 3:
    TELEX; <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-934-455-162
                                                                                                                                                                                                                                          US-09-828-423-3
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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sw model using protein search, OM protein September 15, 2003, 17:18:16 ; Search time 12.6 Seconds
(without alignments)
213.708 Million cell updates/sec Run on:

US-09-544-664-55 148

1 KNLWAAQRYGRELRRMSDEFEGSFKGLK 28 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence:

283308 segs, 96168682 residues Searched: 283308 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	bad protein - mous	inter-alpha-trypsi	$\overline{}$	inter-alpha-inhibi	2-dehydro-3-deoxy-	floral homeotic pr	spermidine/putresc	able thr	DNA-directed RNA p	glycerol-3-phospha	conserved hypothet	Ig kappa chain - h	annexin P35 - maiz	transforming prote	oxidoreductase, so	threonine synthase	hypothetical prote	Antho-RFamide neur				oxoglutarate dehyd		1	Antho-RFamide prec	orin	probable polyamine	inter-alpha-trypsi	conserved hypothet
	dī.	A55671	JC5575	D70760	S54354	538185	A42095	C84338	A96753	A81393	AI1210	E83517	S40376	T02975	C36365	F72289	T08545	T24806	A39172	T09486	\$43852	G82308	F82668	B96695	T02961	A44308	829899	T35440	ΧH	G69510
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dЮ (	Query Match		(*)	""	(.,	٠٠,	٠.,	(-1	(-)	***	33.4	33.1	32.8	32.8	32.4	32.4	32.4	32.4	32.1	32.1	31.8	31.8	31.8	31.8	31.4		31.1	31.1		
	Score	,	54	53	53	52	51	50	50	20	49.5	49	48.5	48.5	48	48	48	48	47.5	47.5	47	47	47	47	46.5	46.5	46	46	919	45.5
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conserved hypothet	probable secreted	hypothetical prote	NADH dehydrogenase	excinuclease ABC c	photosystem II oxy	manganese-stabilzi	conserved hypothet	conserved hypothet	hypothetical prote	sodium ion pump ox	oxaloacetate decar	oxaloacetate decar	oxaloacetate decar	probable membrane	env polyprotein -
AF2859	D97636	C71473	G83314	T36031	S06736	AG2287	F83201	H95406	T31294	B44465	AB0509	AE0909	A28088	S52675	VCLJG4
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327	327	562	905	1014	273	273	295	346	486	591	591	591	296	715	864
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# ALIGNMENTS

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Dad protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Musmar=1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C;Accession: A55671
R;Yang, E; Zha, J; Jockel, J; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
C[81] 80, 285-291, 1995
A;Fitle: Bad, a heterodimeric partner for Bcl.x-L and Bcl.2, displaces Bax and pa;Feference number: A55671
A;Fitle: Bad, a heterodimeric partner for Bcl.x-L and Bcl.2, displaces Bax and pa;Feference number: A55671
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-204 < XAN>
A;Residues: 1-204 < XAN>
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100.0%; Pred. No. 1.2e-12;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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140 NLWAAORYGRELRRMSDEFEGSFKGL 165 2 NLWAAQRYGRELRRMSDEFEGSFKGL 27 ŏ qq

inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster C; Species: Mesocricetus auratus (golden hamster)
C; Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000
C; Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 20-Jun-2000
C; Accession: 10575; Potel 1987
B; Nakatani, T.; Sizuki, Y.; Yamamoto, T.; Sinohara, H.
J; Biochem. 122, 71-82, 1997
A; Title: Molecular cloning and sequencing of CDNAs encoding three heavy-chain precurs sin inhibitor heavy chain family. 7420688; PMID:9276673
A; Reference number: JC5574; MUID:97420688; PMID:9276673

A;Molecule type: mRNA A;Residus: 1-946 <NRAX> A;Cross-references: DDBJ:DB9286; NID:g1694689; PIDN:BAA13939.1; PID:g1694690 A;Experimental source: liver

A,Accession: PC4485
A;Molecule type: protein
A;Residuee: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important role for panceatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;261-264,717-916/Disulfide bonds: #status predicted

36.5%; Score 54; DB 2; Length 946; 34.6%; Pred. No. 11; Query Match Best Local Similarity

a

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42095; S52633; T47593
R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is A;Reference number: A42095; MUID:92154682; PMID:1346756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-370 <AIG)
A; Cross-references: BEBL:236118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBRZ
A; Cross-references: BEBL:236118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBRZ
R; Kuenzler, M.; Paravicini, G.; Byli, C.M.; Irniger, S.; Braus, G.H.
Gene 113, 67-74, 1992
Gene 113, 67-74, 1992
A; Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
A; Reference number: JN0322; MUID:922225349; PMID:1348717
A;Title: The complete sequence of a 6794 bp segment located on the right arm of chron A;Reference number: S38185; MUD:94078675; PMID:8256522 A;Accession: S38185 A;Accession: S38185 A;Etatus: translation not shown A;Nolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-370 <ALJ>
A; Residues: 1-370 <ALJ>
A; Cross-references: EMBL: 236118; NID:9536664; PIDN:OAA85212.1; PID:9536665; MIPS:YBR; R; Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F. submitted to the Protein Sequence Database, August 1994
A; Reference number: 845940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifur A, Reference number: A48651; WOID:93374850; PMID:8366040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Description: aldehyde-lyase; carbon-carbon lyase
A.Pathway: aromatic amino acid biosynthesis; shikimate pathway
A.Note: first step in shikimate pathway
C.Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C.Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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N,Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                 A; Residues: 1-170 <DOI>
A; Residues: 1-170 <DOI>
A; Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102
R; Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kuenzler, M.; Balmelli, T.; Bgli, C.M.; Paravicini, G.; Braus, G.H.
J. Bacteriol. 175, 5548-5558, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SGD:ARO4
A;Cross-references: SGD:S0000453; MIPS:YBR249c
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DLEAAQEYALRIKKLSDELKG 100
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A; Residues: 1-204,208-370 <KUE>
A; Cross-references: EMBL:X61107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 352-370 <KU2>
A;Cross-references: GB:X61107
                                                                                                                                                                                                                                                                                                              A; Reference number: S45906
A; Accession: S46126
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-370 <ALJ>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 2R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
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A42095
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C;Species: Saccharomyces cerevisiae
C;Aate: 31-Dec-1993 #text_change 03-Jun-2002
C;Aate: 31-Besides: S46126; S46130; JN0322; B48651
R;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Scassion: D70760
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1.223 <COLD
A;Residues: 1.223 <COLD
A;Cross-references: GB:Z/4025; GB:AL123456; NID:93261586; PIDN:CAA98415.1; PID:e1299911;
A;Experimental source: strain H37Rv
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
Cispecies: 544364
A.Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: A.Reference number: 554353; MUID:95194326; PMID:7534067
A.Reference number: 554353; MUID:95194326; PMID:7534067
A.Recession: 554354
A.Status: preliminary; nucleic acid sequence not shown
A.Rolecule type: mRAA
A.Residues: 1-946 < CCHA>
A.Residues: 1-946 < CCHA>
A.Residues: EMBL:X70392; NID:g695633; PIDN:CAA49842.1; PID:g695634
Cisperfamily: inter-alpha-trypsin inhibitor complex component II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s.
                                                                                                                                                                                                                                                                                            hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17.041-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70760
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Darbiss, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
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Pred. No. 16;
5; Mismatches 12; Indels
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       Indels
   12;
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212 NVWIIEPQGMRFLHVPDTFEGHFQGV 237
                                                                                                      Score 53;
Pred. No.
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                                                                  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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5.
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58.8%;
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Best Local Similarity 34.6%;
Matches 9; Conservative
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Best Local Similarity 58.83
Matches 10; Conservative
       Conservative
6
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Circueszuni Asolu (A.C.) Ecker, J.R.; Pelm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.B.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, G.A.; Li, Y.H.; Liu, S.Y.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, K.Er, W., V., V., V., G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 01-Mar-2002
C;Accession: A11210
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloe
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi
D; Jones, L.M.; Karst, U.
Science 204, 849-882, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A81393
Psarkhili, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chi.
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba.
Nature 403, 665-668, 2000
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A; Status: preliminary
A; Modeoule type: DNA
A; Residues: 1-1378
A; Residues: 1-1378
Cxross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75116.1; PID:g69-A; Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed RNA polymerase (EC 2.7.7.6) beta chain Cj0478 [imported] - Campylobacte. C.Species: Campylobacter jejuni
C.Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A. Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 2; Length 516; Pred. No. 23;
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A;Gene: rpoB; Cj0478
C;Superfamily: DMR-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----EFEGSFKGL
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Matches, 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-516 <STO>
                                C; Accession: A96753
                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A96753
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AI1210
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A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUD:20504483; PMID:11016950
A; Accession: C84338
A; Status: preliminary
                                                   A; Experimental source: perals, stamens
A;Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
R;Okamoto, H.; Yamo, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid A;Reference number: S52633; MuID:95036018; PMID:7948893
                                                                                                                                                                                                                                                                                                                                                                                             R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A;Reference number: 224469
A;Accession: T47593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Reywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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A)Cross-references: GB:AE004437; NID:g10581314; PIDN:AAG20071.1; GSPDB:GN00138
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spermidine/putrescine ABC transporter [imported] - Halobacterium sp. NRC-1
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                             A;Cross-references: GB:M86357; NID:g166607; PIDN:AAA32740.1; PID:g166608
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Pred. No. 7.3;
3; Mismatches 4; Indels
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C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1.1.232 <BLO>A; Cross-references: EMBL:AL132971
A; Experimental source: cultivar Columbia; BAC clone T12E18
C; Genetics:
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Pred. No. 17;
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A; Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A;Note: T12E18.30
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1; Mismatches
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76.9%;
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Local Similarity 44.4%;
les 12; Conservative
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ELRRISDAVEGSF 209
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R;Bloecker, H.; Mewes, H.W.; I
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Best Local Similarity
Matches 10; Conserv
A; Residues: 1-232 <JAC>
                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <OKA>
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A; Molecule type: DNA
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Ricasale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 654-6653, 1990
A/Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which expression: 4, Reference number: A36365; MvID:91061774; PMID:1701021
A. Accession: C36365
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                                                                                                                                                                                                                                                                                                                                                C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T02975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rhizomucor racemosus
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C;Accession: C36365
       Gaps
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Bant Physiol. 1312, 1391-1395, 1996
A; Title: CDNA isolation and gene expression of maize annexins P33 and is A; Reference number: 214796; MUID:97092863; PMID:8938425
A; Accession: T02975
A; Accession: T02975
A; Molecule type: mRNA
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                                                                              -SDEFEGSFKG
                                                                                                                                        58 WFRQRPGRSPRRLIYNVSKRDSGVSDRFSGSGSG
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Pred. No. 23;
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10; Conservative
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Best Local Similarity 47.6
Matches 10; Conservative
                                                                           4 WAAQRYGRELRRM---
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A;Molecule type: DNA
A;Residues: 1-206 <CAS
A;Cross-references: GB:M55177
   13; Conservative
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Matches 10; Conserv
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE004091; NID:g9946936; PIDN:AAG04420.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Fseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: E83517
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
                     A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AI1210
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-127 <GLA
A/Residues: 1-127 <GLA
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C/Genetics:
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C/Status: Appl
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A; Residues: 1-134 < KLES
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C; Superfamily: immunoglobulin V region: immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-113/Domain: immunoglobulin homology < INM>
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36.4%; Pred. No. 6.5;
tive 6; Mismatches 10;
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Pred. No.
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A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1031
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B; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.; Nature 399, 333-329, 1999
A; Pride. Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A; Reference number: A72209
A; Pride. Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A; Reference number: A72209
A; Pride. Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A; Reference number: A72209
A; Pride. Evidence for lateral gene transfer PMID: 10360571
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|           | Description           | Q61337 mus musculu | 035147 rattus norv | Q92934 homo sapien |            | mus mu        |      | rhodod     | 062991 rhododendro |            | P35632 arabidopsis |            |            |            |            |            |            |            |            |            | 043521 homo sapien |            | Q16994 anthopleura |            |            |            |            |            |            |            | Q13049 homo sapien |           | Q9nyf5 homo sapien | m          |
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| SUMMARIES | ID                    | BAD_MOUSE          | BAD_RAT            | BAD_HUMAN          | ITH2_MESAU | ITH2_MOUSE    |      | MATK_RHOFR | MATK_RHOTS         | AROG_YEAST | AP3_ARATH          | CE05_MOUSE | RPOB_CAMJE | RWUC_PSEAE | RAS3_RHIRA | 6PGL_THEMA | THRC_SOLTU | THRC_ARATH | FWRA_CALPA | MATK_LOIPR | BIM_HUMAN          | PRFA_POLPE | FMR2_ANTEL         | FMR1_ANTEL | ITH2_HUMAN | UVRA_STRCO | PSBO_ANASP | SNF4_KLULA | DCOA_SALIY | DCOA_KLEPN | HT2A_HUMAN         | ENV_SIVAT | CE05_HUMAN         | LML1_CAEEL |
|           | DB                    | Н                  |                    | Н                  | Н          | <del></del> 1 | Н    | Н          | <del></del> 1      | -1         | Н                  | гН         | H          | ↔          | Н          | H          |            | Н          | H          | ~1         | ,— <u>;</u>        | Н          | -4                 | Н          | -          | -1         | П          | <b>~</b>   | Н          | ~          | Н                  | Н         |                    | -          |
|           | Ouery<br>Match Length | 204                | 202                | 168                | 946        | 946           | 206  | 506        | 206                | 370        | 232                | 851        | 1378       | 453        | 202        | 220        | 519        | 526        | 334        | 507        | 198                | 287        | 429                | 435        | 946        | 1014       | 273        | 328        | 290        | 595        | 653                | 865       | 915                | 1535       |
| ۵P        | Query<br>Match        | 66                 |                    | 77                 | 36         | 35            | 35   | 35         | സ                  | ഷ          | 34                 | 34         | 33         | 33         | 32         | 32         | 32         | 32         | 33         | 32         | 31                 | 31         | 37                 | 31         |            | 30         | 30         | 30         | 30         | 30         | 30                 |           | 30.4               |            |
|           | Score                 | 138                | 138                | 114                | 54         |               | 52.5 | (A         | (1                 | 52         | 51                 | 51         | 50         | 49         | 48         | 48         | 48         | 48         | 47.5       | 47.5       | 47                 | 47         | w                  | 46.5       |            | 45.5       | 45         | 45         | 45         | 45         | 45                 | 45        | 45                 | 45         |
| i         | Result<br>No.         | н                  | 2                  | m                  | 4          | Ŋ             | 9    | 7          | 80                 | თ          | 10                 | 11         | 12         | 13         | 14         | 15         | 16         | 17         | 18         | 19         | 20                 | 21         | 22                 | 23         | 24         | 25         | 26         | 27         | 28         | 29         | 30                 | 31        | 32                 | 33         |

| homo sapien | lilium tsin               | salmonella<br>mus musculu | rattus norv | escherichia<br>escherichia | salmonella | salmonella | thermotoga |
|-------------|---------------------------|---------------------------|-------------|----------------------------|------------|------------|------------|
| Q9nu22      | 29393<br>099193<br>P33602 | P33900                    | 088498      | Q8X906<br>P50465           | Q8z8d2     | 08zdne     | 033925     |
|             |                           |                           |             |                            |            |            |            |
| MDN1_HUMAN  | MATK_LILIS<br>NUOG_ECOLI  | NUOG_SALTY<br>BIM MOUSE   | BIM_RAT     | END8_ECO5/                 | END8_SALTI | END8_SALTY | SYM_THEMA  |
| ~ ~         |                           |                           | Н.          | <del></del>                | Н          | г          | Н          |
| 5596        | 512                       | 907                       | 196         | 7 6 7<br>7 6 7<br>7 6 7    | 262        | 262        | 629        |
| 30.4        | 30.1                      | 30.1                      | 29.7        | 200.7                      | 29.7       | 29.7       | 29.7       |
| 45          | 44.5                      | 44.5                      | 77          | † †<br>† †                 | 44         | 44         | 77         |
| 34<br>35    | 36                        | 8 6<br>8 8                | 40          | 4<br>4<br>7                | 43         | 44         | 45         |

|                                         | ろろろろろのままままます。<br>中にのてのののこのできまし                                | N N N N O O O O O O O O O O O O O O O O                                                                           | 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                    | 00000000000000000000000000000000000000            | еенанаена                        | MAT<br>MAT<br>MAT<br>NUO<br>NUO<br>NUO<br>BIM<br>BIM<br>END<br>END | MDN1_HUMAN MATK_GAUPR MATK_LILIS NUOG_ECOLI NUOG_SALIY BIM_MOUSE BIM_MOUSE BIM_RAT ENDB_ECOST | PPR<br>T T T T T T T T T T T T T T T T T T T |                                                                                                                                                                                                                                                                                                         | 095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910<br>095910 | homo sapi<br>gaultheri<br>lilium ts<br>escherich<br>salmonell<br>mus muscu<br>rattus no<br>escherich<br>escherich<br>salmonell |  |
|-----------------------------------------|---------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------|---------------------------------------------------|----------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|--|
|                                         | 45                                                            | <b>7</b>                                                                                                          | υ.                                                       | 629                                               |                                  | SYM                                                                | THEM                                                                                                                                                                                                                                                                                                                      | hema<br>Ignments                             |                                                                                                                                                                                                                                                                                                         | 033925                                                                                                                                                       | thermotoga                                                                                                                     |  |
| SOL                                     | ULT 1<br>_MOUSE<br>BAD_N                                      | TOUSE                                                                                                             | STS                                                      | STANDARD;                                         |                                  | D.                                                                 | RT;                                                                                                                                                                                                                                                                                                                       | 204                                          | AA.                                                                                                                                                                                                                                                                                                     |                                                                                                                                                              |                                                                                                                                |  |
| SE TE CO                                | 2613:<br>01-NC<br>01-NC<br>28-FI<br>BCL2-                     | Q61337;<br>01-NOV-1997 (Rel. 3<br>01-NOV-1997 (Rel. 28-FEB-2003 (Rel. 8<br>BC12-antagonist of 6) (Bc1-xL/Bc1-2 as | (Rel.<br>(Rel.<br>(Rel.<br>ist of                        | 30,1,0,8                                          | eat<br>st<br>st<br>dea<br>ted    | ed)<br>sequ<br>anno<br>th (                                        | Created) Last sequence update) Last annotation update il death (BAD) (Bcl-2 b) coiated death promoter).                                                                                                                                                                                                                   | updat<br>n upc<br>(Bcl-                      | ,<br>Inding                                                                                                                                                                                                                                                                                             | component                                                                                                                                                    |                                                                                                                                |  |
| X 8 8 8 8 X                             | BAD (<br>Mus r<br>Eukaj<br>Mammik<br>NCBI                     | DR BBC6.<br>nusculus<br>ryota; M<br>alia; Eu                                                                      | 16.<br>Lus (Mouse<br>Metazoa;<br>Eutheria;               | (a)                                               | dat<br>nti                       | a;;                                                                | raniata<br>ciurogna                                                                                                                                                                                                                                                                                                       | ta; Ve<br>gnathi                             | ebrata;<br>Muridae;                                                                                                                                                                                                                                                                                     | Euteleos<br>Murinae                                                                                                                                          | tomi;<br>; Mus.                                                                                                                |  |
| RN<br>RP<br>RX<br>RT<br>RT              | SEQUI<br>SEQUI<br>TISSU<br>MEDL:<br>Yang<br>"Bad<br>Prom(Cell | SNCE FRC<br>JE=Brain<br>INE=9513<br>E., Zha<br>E., a hete<br>otes cel                                             | M N.A.<br>16361;<br>16361;<br>107.<br>2rodime<br>11 deat | 1 Thymus; PubMed=78 Jockel J., meric partn tth."; | ;<br>=78<br>J.,<br>rtn           | 34748<br>Bois<br>er fk                                             | 8;<br>or Bc                                                                                                                                                                                                                                                                                                               | H., J                                        | hompson C.B<br>and Bcl-2,                                                                                                                                                                                                                                                                               | , Korsmeyer<br>displaces Baz                                                                                                                                 | eyer S.J.;<br>s Bax and                                                                                                        |  |
| : # # # # # # # # # # # # # # # # # # # | MEDL:<br>Del l<br>"Int                                        | PHORYLAI<br>INE=9802<br>Peso L.,<br>erleukin<br>se Akt."                                                          | Gonza<br>1.3-inc                                         | AND MUT<br>PubMed<br>alez-Ga<br>Auced p           | AGE<br>=93<br>rci                | NESI<br>8117<br>a M.<br>phor                                       | S OF<br>8;<br>Pag<br>ylati                                                                                                                                                                                                                                                                                                | SER-1<br>e C.,<br>on of                      | .12 AND SER-<br>Herrera R.<br>EAD throug                                                                                                                                                                                                                                                                | ez<br>pr                                                                                                                                                     | G.;<br>otein                                                                                                                   |  |
| RRRRR                                   | Sciel<br>[3]<br>MUTA(<br>MEDI:<br>Datta                       | SENESIS<br>INE=204C                                                                                               | 687-68<br>OF SEI<br>3302;<br>Katsov                      | 39(1997<br>RINE RE<br>PubMed                      | ).<br>SID=10<br>u L              | UES.<br>9490<br>., P                                               | 26;<br>etros                                                                                                                                                                                                                                                                                                              | A.,                                          | Fesik S.W.,                                                                                                                                                                                                                                                                                             | ×                                                                                                                                                            | В.,                                                                                                                            |  |
| RT<br>RT<br>F                           | #14-                                                          | 3-3 prot<br>domain p                                                                                              | E.;<br>eins a<br>phospho                                 | and sur<br>orylati                                | viv<br>on.                       | a<br>∴ ×                                                           | inase                                                                                                                                                                                                                                                                                                                     | S COC                                        | perate to i                                                                                                                                                                                                                                                                                             | rat<br>T                                                                                                                                                     | e BAD by                                                                                                                       |  |
| 188888                                  | }-                                                            | FUNCTION<br>Sinding<br>of heter                                                                                   | to Bcl                                                   | notes c<br>L-x(L),<br>rizatio                     | ell<br>Bc<br>n o                 | dea<br>1-2<br>f th<br>y of                                         | th. Sand Bese past.                                                                                                                                                                                                                                                                                                       | ucces<br>cl-w,<br>rotei<br>x(L),             | ssfully comp<br>thereby af<br>ns with BAX                                                                                                                                                                                                                                                               | ig<br>re<br>me                                                                                                                                               | the<br>the leve<br>rerse th                                                                                                    |  |
| 288888                                  | 1 1                                                           | Appears and the SUBUNIT: K(L), Bc                                                                                 | apopto Forms 112/Se                                      | t as a<br>otic pa<br>s heter<br>od Bcl-<br>er-136 | thw<br>odi                       | ays.<br>ays.<br>mers<br>Also<br>spho                               | tween<br>with<br>bind<br>rylat                                                                                                                                                                                                                                                                                            | grow<br>the<br>s pro                         | anti-apopto<br>tein S100Al<br>orm binds 14                                                                                                                                                                                                                                                              | eceptor s<br>tic prote<br>0 (By sin<br>-3-3 prot                                                                                                             | cor signaling roteins, Bcl-similarity). proteins.                                                                              |  |
| 3888888                                 |                                                               | SOBCELLO<br>SOMAIN:<br>SOMAIN:<br>BAX for<br>with ant                                                             | Intact<br>Intact<br>their<br>i apor                      | on, loc<br>bh, loc<br>BH3 d<br>pro-ap<br>pro-ap   | ate<br>oma<br>opto<br>opto<br>on | s to<br>in i<br>otic<br>otic<br>bers                               | the the action of t                                                                                                                                                                                                                                                                                                       | cytop<br>cytop<br>wired<br>vity<br>he Bd     | phosphorylation, locates to the cytoplasm.  -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAR BAX for their pro-apoptotic activity and for their int with anti-apoptotic members of the Bcl-2 family.  -!- PIM: Phosphorylated on Ser-112 in response to survival chacked by the Bcl-2 family. | ", BID, BAK, BAD AND their interaction ily."                                                                                                                 | SAD AND action cimuli.                                                                                                         |  |
| 1888                                    |                                                               | with 14-<br>phosphorto the r                                                                                      | 3-3 pr                                                   | coteins<br>on at S                                | er - 1                           | his<br>155,<br>(L)                                                 | inter<br>inter<br>a si                                                                                                                                                                                                                                                                                                    | actic<br>te wi                               | then faci<br>thin the BH<br>comotion of                                                                                                                                                                                                                                                                 | litates the 3 domain, lea                                                                                                                                    | sitation<br>the<br>leading<br>/ival.                                                                                           |  |

a

```
InterPro; IPR000712; Bcl2_BH.
  Apoptosis;
   CONFLICT
  VARSPLIC
  PROSITE;
   MOD_RES
  MOD_RES
   MUTAGEN
  MUTAGEN
   DOMAIN
  EMBL;
  HSSE;
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  ;
0
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 honology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
  S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION; INTERACTS WITH
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
   Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
Interference of BAD (Bcl.xL/Bol-2-associated death promoter)-induced
apoptosis in mammalian calls by 14-3-3 isoforms and Pll.";
Mol. Endocrinol.11:1858-1867(1997).
  D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
   Gaps
   PKB).
PKB).
  ô
  BAD_RAT STANDARD; PRT; 205 AA.
035147; 070256; 099HX1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FFE-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).
   93.2%; Score 138; DB 1; Length 204;
   SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
   PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND
  Indels
   6C2BA910205053F7 CRC64;
   0;
   Pred. No. 2.5e-13;
  SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
   0; Mismatches
   140 NIWAAQRYGRELRRMSDEFEGSFKGL 165
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   BCL-X(L)
   TISSUE=Brain;
MEDLINE=21109372; PubMed=11161472;
   HSSP, 022934; 1G5J.
MGD; MGI:1096330; Bad.
InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
   MEDLINE=98194755; PubMed=9535132;
  Neurosci. Lett. 243:137-140(1998).
   MEDLINE=98034386; PubMed=9369453;
  22080 MW;
   100.0%;
  EMBL; L37296; AAA64465.1; -.
  Phosphorylation.
  Conservative
   BAD.
Rattus norvegicus (Rat)
   1112
1136
1155
1112
1136
155
   PIR; A55671; A55671.
  204 AA;
  Best Local Similarity
Matches 26, Conserv
   SEQUENCE FROM N.A.
  brain.
   TISSUE=Brain
  Apoptosis;
DOMAIN
   SEQUENCE
  Query Match
   MOD_RES
MOD_RES
   MUTAGEN
  the rat
   MOD_RES
  MUTAGEN
  RESULT 2
  BAD_RAT
  SHHHHHHHHBBBBBBBBBBBBHHHH
   ð
  g
```

-> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP

PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
LPRPKSAGTATQNRQSASWTRIIQSWWDRNLGKGGSTPSQ

156 137

166

(BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY). PHOSPHORYLATION (BY PKA AND PKB)

PS01259; BH3; FALSE\_NEG.

Q92934; 1G5J

162 137 156 S->A: NO HETERODIMERIZATION WITH 14-3-3 PROTEINS. NO EFFECT ON HETERODIMERIZATION WITH BCL2 NOR WITH PROTEIN P11.

SDAGGR -> ERRGRK (IN REF. 1). 7AFA71DAE9CF4A81 CRC64;

34 S 22228 MW;

29 205 AA;

S->A: NO EFFECT ON HETERODIMERIZATION WITH 14-3-3 PROTEINS. EVAMFPLRYWTALRRLC (in isoform Beta).

/FTId=VSP 000534

113 137

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Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

"Functional Characterization of two splice variants of rat BAD and
their interaction with Bcl-w in sympathetic neurons.";

Mol. Cell. Neurosci. 17:87-106(2001).

-! FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-xCl, Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-xCl), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-! SUBGNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-xCl), Bcl-2 and Bcl-w. Also binds protein S100A10. The Ser-XIJ/Ser-137 phosphorylated form binds 14-3-3 proteins.

-! SUBCRILUTAR IOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
   DOMAIN: Intext BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

FTM: Phosphorylated on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-13 in response to survival stimuli. Subsequent phosphorylation on Ser-13 interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of RKT/PKB phosphorylation (By
  TISSUB SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more
  -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
   ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
  IsoId=035147-2; Sequence=VSP_000534;
  IsoId=035147-1; Sequence=Displayed;
  EMBL; AF031227; AAC15100.1; -.
EMBL; AF279910; AAF91427.1; -.
EMBL; AF279911; AAF91428.1; -.
  EMBL; AF003523; AAC53374.1; -.
   similarity).
  Name=Alpha;
  Name=Beta;
```

δŏ Q

```
Query Match
  MOD_RES
   DOMAIN
  HELIX
  MIM;
REC TISSUB-Lung;
RX MEDLINE-22388257; PubMed-12477932;
RA STRAUBERGY R.L., Felngold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.E., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
RA Altschul S.E., Zeeberg B., Buetow K.H., Schemer C.F., Bhat N.K.,
RA Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McErnan K.J., Malek J.A., Gunsratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchan J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RY "Generation and initial analysis of more than 15,000 full-length
   .
0
  Yi\bar{n} D.X., Li Z., Huang B., Chen S., Zhou H.; "A human protein that interacts with Bcl-2 and have homology to mouse
   092934; 014803; Created)
01-NOV-1997 (Rel. 35, Created)
15-CCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
BCl2-antagonist of cell death (BAD) (Bcl-2 binding component 5) (Bcl-XL/Bcl-2 associated death promoter) (BCL2-like 8 protein).
BAD OR BBC6 OR BCL2L8.
   Gaps
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
   .:
0
   Ottilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G., Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
"Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
              Score 138; DB 1; Length 205;
  SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
MEDILINE-97083574; PubMed-8929532;
WANG H.-G., Rapp U.R., Reed U.C.;
"Bc1-2 targets the protein kinase Raf-1 to mitochondria.";
   0; Indels
   Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                               100.0%; Pred. No. 2.5e-13; ive 0; Mismatches 0;
  168 AA.
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  SEQUENCE FROM N.A., AND DIMERIZATION.
   PRT;
   TISSUE=Bone marrow;
MEDLINE=98049554; PubMed=9388232;
              93.2%;
   26; Conservative
  STANDARD;
  87:629-638(1996)
   Homo sapiens (Human)
                               Similarity
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  BAD HUMAN
              Query Match
                                Best Local
   Matches
  [9]
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  SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) Gomain.
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) Gomain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
   phosphorylation, locates to the cytoplasm.

TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
BAX for their pro-apoptotic activity and for their interaction
with anti-apoptotic members of the Bcl-2 family.

PTM: Bhosphorylated on Ser-75 in response to survival stimuli.

Subsequent phosphorylation on Ser-99 promotes heterodimerization
with 14-3-3 proteins. This interaction then facilitates the
phosphorylation at Ser-118, a site within the BH3 domain, leading
to the release of Bcl-x(L) and the promotion of cell survival.

Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
major site of protein kinase A (CAPK) phosphorylation (by
                                     Meadows R.P.
  (BY
   (BY
  PHOSPHORYLATION (BY PKA AND PKB) (BY
   PHOSPHORYLATION (BY PKA AND PKB)
  SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
   Score 114; DB 1; Length 168;
   PHOSPHORYLATION (BY PKA AND
MEDLINE-21073561; PubMed=11206074; Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.
  Phosphorylation; Polymorphism; 3D-structure,
  SIMILARITY).
A -> S (in dbSNP:3729933).
/FIId=VAR_015380.
  69FD8D27DDEE3241 CRC64;
   607. GO:0005737; C:cytoplasm; NAS.
GO: GO:0005741; C:mitochondrial outer membrane; 160; GO:0005514; P:protein binding activity; NAS.
GO: GO:0008632; P:apoptotic program; TAS.
GO: GO:0008617; P:induction of apoptosis; NAS.
  SIMILARITY
   SIMILARITY
   EMBL; U66879; AAB36516.1; ALT_FRAME.
EMBL; AF031523; AAB72092.1; --
EMBL, AF031523; AAB88124.1; --
EMBL; BC001901; AAH01901.1; --
PDB; 1G5J; 07-FEB-01.
  InterPro, IPR000712; Bcl2_BH.
PROSITE; PS01259; BH3; FALSE_NEG
   18392 MW;
   77.0%;
   124
75
  66
  118
   107
   Genew; HGNC:936; BAD.
MIM; 603167; -.
   168 AA;
  9
   118
   107
   106
  similarity
   Fesik S.W.;
  Apoptosis;
  SEQUENCE
   MOD_RES
  MOD_RES
   VARIANT
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4

SM00327; VWA; 1.

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SMART;
  1-
   RESULT 5
                            NAME OF THE PROPERTY OF THE PR
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  g
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  ö
  Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor
   SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HI, H= OR H3) AND ONE LIGHT CHAIN, BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND BIKUNIN, AND PRE-ALPHA-INTHIBITOR (P-ALPHA-LI) OF H3 AND PRE-HEAVY CHAINS ARE INTERLINED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASSPARAME (BY
  Gaps
   J. Biochem. 120:145-152(1996).

-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZATION, SYMPHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
  [2]
SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
   15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoni;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
  Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian
  ..
0
  Indels
7.6e-10;
  946 AA.
   -!- SIMILARITY: BELONGS TO THE ITH FAMILY.
-!- SIMILARITY: Contains 1 VWFA domain.
  Mismatches
  or send an email to license@isb-sib.ch).
                          SO.
   Mesocricetus auratus (Golden hamster).
  103 NLWAAQRYGRELRRMSDEFVDSFK 126
   2 NLWAAQRYGRELRRMSDEFEGSFK 25
  PRT;
                            Pred.
   MEDLINE=97420688; PubMed=9276673;
   MEDLINE=97018241; PubMed=8864857;
  ;
0
   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
                   91.78;
  heavy chain family.";
J. Biochem. 122:71-82(1997).
   PIK; JC59/5; JC55/9.
InterPro; IPR006587; VII.
InterPro; IPR002035; VWE_A.
PÉRN; PP00092; VWR; I.
SMART; SM00609; VII; I.
  hamster urine and plasma.",
   EMBL; D89286; BAA13939.1;
  Conservative
  STANDARD;
                     Similarity
  (Rel.
  SEQUENCE FROM N.A.
  NCBI_TaxID=10036;
  SIMILARITY)
   SIMILARITY)
   IISSUE=Plasma;
  JC5575;
   Mesocricetus
   TISSUE=Liver
  22;
   ITH2_MESAU
                        Best Local
  TTH2_MESAU
   Matches
   AND
   엄
   ŎΣ
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   BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
   STRAIN=CSTBL/6N; TISSUB-Liver;

MEDLINE-95194326; PubMeda-7534067;

Chan P., Risler J. L., Raquenez G., Salier J.-P.;

Chan P., Risler J. L., Raquenez G., Salier J.-P.;

"The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcription in liver and brain.";

Biochem. J. 306:505-512(1995).

-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING RROTEIN BETWERN HYALURONAN AND CHERK X PROFIEN, INCLUDING THOSE ON CELL SURFACES IN TISSUBS TO REGILATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
   Gaps
  SUBGUNIT: I'ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKGUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKGUNIN, INYER-ALPHA-LIKE INHIBITOR (1-ALPHA-I) OF H2 AND BIKGUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKGUNIN.
  -!- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
-!- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
  CROSS-LINK SITE
   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-PEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
chain H2) (Inter-alpha-inhibitor heavy chain 2).
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  (POTENTIAL).
  N-LINKED (GLCNAC. . .) (POTENTIAL)
   ;
0
  (POTENTIAL
                           Repeat; Signal; Multigene family;
   Score 54; DB 1; Length 946;
Pred. No. 4.3;
   Indels
  CA8BF565458E7B2E CRC64;
  N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
   CHONDROITIN 4-SULFATE,
   12;
   V -> Y (IN REF. 2).
E -> I (IN REF. 2).
  (BY SIMILARITY)
  946 AA
   -!- SIMILARITY: BELONGS TO THE ITH FAMILY.
   5; Mismatches
  SIMILARITY
  212 NVWIVELQGMRFLHVPDTFEGHFQGV 237
   POTENTIAL
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  106580 MW;
  36.5%;
   34.6%;
PROSITE; PS50234; VWFA; 1.
Serine protease inhibitor;
  Best_Local Similarity 34.6
Matches 9; Conservative
  STANDARD;
   946
468
1118
263
263
702
   510
   Mus musculus (Mouse)
  595
946 AA;
   SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
   SIMILARITY).
  SIMILARITY)
   Glycoprotein.
SIGNAL
  ITH2 MOUSE
  CARBOHYD
  CARBOHYD
  CONFLICT
   SEQUENCE
  Query Match
   CARBOHYD
  CARBOHYD
  CONFLICT
  BINDING
   PROPEP
DOMAIN
  PROPEP
  CHAIN
   ITIHZ.
  ITH2_MOUSE
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   Gaps
   Chloroplast.
Bukaryotka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceaa; Ericoideae, Rhodoreae; Rhododendron.
   -1- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-1- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
   7:
   SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Iukawa T.;
  Score 52.5; DB 1; Length 506; Pred. No. 3.6; 5; Mismatches 8; Indels
  DB 1; Length 506;
   Indels
  "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matk sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
  506 AA; 60534 MW; ADA44B25E92436E8 CRC64;
  CFEA926307DAC85E CRC64;
   ώ
ώ
   41, Last sequence update)
41, Last annotation update)
  | :||| :||| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
   391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  35.5%; Score 52.5; DE 37.5%; Pred. No. 3.6; ive 5; Mismatches
  506 AA.
  506 AA.
   EMBL; AB012741; BAA25862.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
        EMBL; AB012751; BAA25872.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N, 1...
   Rhododendron ferrugineum (Alpenrose).
  PRT;
   Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequ
28-FEB-2003 (Rel. 41, Last anno
   Chloroplast.
A; 60412 MW;
   mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60534 MW;
  35.5%;
37.5%;
  Maturase K (Intron maturase)
  Query Match
Best Local Similarity 37.55
Matches 12; Conservative
  Query Match 35.5
Best Local Similarity 37.5
Matches 12; Conservative
  STANDARD;
  STANDARD;
   mRNA processing; Ch.
SEQUENCE 506 AA;
  NCBI_TaxID=49622;
  MATK_RHOTS
ID MATK_RHOTS
AC 062991;
  MATK_RHOFR
   062984;
  MATK_RHOFR
   RESULT 8
  RESULT 7
              SO WE WE DR.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ;
0
   BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
H2.
  Gaps
  N-LINKED (GLCNAC, . .) (POTENTIAL),
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
(BY SIMILARITY).
1; 40DB6716433ED9DC CRC64;
  Chillorogras.
Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
  -!- FUNCTION: Probably assists in splicing chloroplast group II
  ·;
   introns (By similarity).
-i- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
  PROSITE; PS50234; VWFA; 1. Serine protease inhibitor; Repeat; Signal; Multigene family;
  [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
  DB 1; Length 946;
  12; Indels
   "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
   Last sequence update)
Last annotation update)
  5; Mismatches
   506 AA.
   BY SIMILARITY. VWFA.
  Score 53;
Pred. No. (
  212 NVWIIEPQGMRFLHVPDTFEGHFQGV 237
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   POTENTIAL
   PRT;
  Ledum palustre (Wild rosemary).
   MM:
  Created)
  PIR; S54354; S54354.
MGD; MGI-96619; ILth2.
InterPro; IPR006587; VWF_A.
Ffam: PF00092; vwa; 1.
SMART; SW00692; vva; 1.
SMART; SW00327; VWA; 1.
   Maturase K (Intron maturase).
  35.8%;
   EMBL; X70392; CAA49842.1; -.
   105927
  9; Conservative
   STANDARD;
   946
468
1118
263
702
  (Rel. 42, (Rel. 42, (Rel. 42,
   946 AA;
  Query Match
Best Local Similarity
  NCBI_TaxID=75583;
   703
308
1118
263
702
   19
   SUBFAMILY
   Glycoprotein.
SIGNAL
  15-SEP-2003
15-SEP-2003
   15-SEP-2003
  Chloroplast
   MATK_LEDPA
   DOMAIN
CARBOHYD
  CARBOHYD
CARBOHYD
   SEQUENCE
  BINDING
   PROPEP
  PROPEP
  CHAIN
   MATK_LEDPA
  Matches
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Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
  Best Local Similarity
Matches 10; Conserv
  HSSP; P00886; 1QR7
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  first step.
  STRAIN=S288c;
       Kuenzler M.;
   80
  Query Match
   RESULT 10
   AP3_ARATH
  ò
   g
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   1;
   MEDINE-9225349; PubMed=1348717;
Mentaler M., Paravicini G., Egli C., Irniger S., Braus G.H.;
"Cloning, primary structure and regulation of the ARO4 gene, encoding
the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
   Gaps
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoldeae; Rhodoreae; Rhododendron. NCBL_TaxID-49629;
  01-CCT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
   "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matk sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-:- FUNCTION: Probably sasists in splicing chloroplast group II introns (By similarity).
-:- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
   35.5%; Score 52.5; DB 1; Length 506; 37.5%; Pred. No. 3.6; ive 5; Mismatches 8; Indels 7
   ŚEĞUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
  60569 MW; AEE12FF8809C223E CRC64;
   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
  Last sequence update)
Last annotation update)
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   370 AA.
   synthase from Saccharomyces cerevisiae."; Gene 113:67-74(1992).
   EMBL; AB012750; BAA25871.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
   Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK.N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60569 MW; AEE
     Created)
  Maturase K (Intron maturase).
  ARO4 OR YBR249C OR YBR1701
   Rhododendron tsusiophyllum
   12; Conservative
   STANDARD;
28-FEB-2003 (Rel. 41, 28-FEB-2003 (Rel. 41, 28-FEB-2003 (Rel. 41,
   [2]
REVISIONS TO 205-207.
  Best Local Similarity
   SEQUENCE FROM N.A.
  NCBI_TaxID=4932;
  SUBFAMILY.
  Chloroplast.
   AROG YEAST
  Yukawa T.;
   Query Match
  P32449;
   AROG_YEAST
   Matches
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  Floral homeotic protein APETALA3.

APS OR ATSG54340 OR T12E18_30.

Arbidopsis thaliana (Mouse-eat oress).

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
MEDLINE-94078675; PubMed-8256522; Doignon F., Biteau N., Aigle M., Crouzet M.; Withe complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUT
  Gaps
   SGD; S0000453; ARO4.
GG; GG:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .;
Interpro; IPR006219; AroFGH.
Interpro; IPR006218; DAHBL/KDSA.
  ENZYME REGULATION: INHIBITED BY TYROSINE.
PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
  AP3_ARATH STANDARD; PRT; 232 AA.
P35632; Q39003; Q8LB79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SQ22; Q9SX13;
   0;
  -!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
   Length 370;
   Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
   6; Indels
   1;
   01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
  35.1%; Score 52; DB ilarity 47.6%; Pred. No. 3; Conservative 5; Mismatches
   DLEAAOEYALRIKKLSDELKG 100
  22
  ProDom; PD005060; Arofgu; 1.
TIGRFAMS; TIGR00034; arofgu; 1.
  Pfam; PF00793; DAHP_synth_1; 1.
  2 NLWAAQRYGRELRRMSDEFEG
   EMBL, X61107, CAA43419.1, -..
EMBL, L20296, AAA65607.1; -.
EMBL, Z36118; CAA85212.1; -.
PIR, S38185, S38185.
   duTPase in a yeast.";
Yeast 9:1131-1137(1993).
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EXUGENCE FROM M. A.

RADINE=21016720; PubMed=11130713;

REDINE=21016720; PubMed=11130713;

RADINE=21016720; PubMed=11130713;

RA FARTHEADER M., Reder H., Perez-Alonso M., Obermaier B., Balanoubat M., Lemcke K. Bloecker H., Perez-Alonso M., Obermaier B., Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., Rad Delseny M., Boutry M., Artiguenave F., Robert C., Brotter P., Rad Wincker P., Cattolico., Walsenbach J., Saurin W., Oberier F., Schaefer M., Maeller-Auer S., Gabel C., Fuchs M., Benes V., RA Wiedelmann R., Kranz H., Voss H., Holland R., Bradt P., Nyakatura G., Radelmann R., Kranz H., Voss H., Holland R., Simionati B., Rooriet M., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Radelmann R., Kranz H., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Radelman R., Maarse A.C., Alonare J.-D., Cotterwaelder B., Duchemin D., R. Raichelt J., Scharfe M., Schoen O., Bargues M., Tarol J., Climent J., Rade Haan M., Maarse A.C., Alonare J.-D., Cotter R., Caecuberta B., Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., Ramnhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Wawer K. R., Nittseber J., Sallers P., Gill J.E., Feldblyum T.V., R. Rooney T., Nierman W.C., Salzberg S.L., White O., Venter J.C., R. Frass C. M., Kaneko T., Nakamura Y., Sacto S., Kato T., Asamizu E., Ramondo S., Kimura T., Ideaswa K., Kawashima K., Kishida Y., Ramanda M., Makaswa C., Kohara M., Matsumoo M., Matsumo A., Muraki A., Nakasaki N., Shinpo S., Takeuchi C., Wada T., Ramada M., Makasumo B., Makasaki N., Shinpo S., Takeuchi C., Wada T., R., Nakajama M., Sabande A., Tabata S., Makasaki N., Shinpo S., Tabata S., Makasaki N., Sabata S., Sato S., Sato S., Sato S., Sato S., Sato S., Sato S., Sato S., Sato S., Sato S., Sat
   Jack T., Brockman L.L., Meyerowitz E.M.; "The Annoctic gene APETALA" of Arabidopsis thaliana encodes a MADS box and is expressed in petals and stamens."; cell 68:683-697(1992)
  Purugganan M.D., Suddith J.I.; "Molecular population genetics of floral homeotic loci: departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thaliana."; Genetics 151:839-848(1999).
  "Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of
  SEQUENCE FROM N.A., AND VARIANTS.
STRAIN-cv. Bla-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2, cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0, cv. Gr-3, cv. Jl-8, cv. Ka-1, cv. Kent, cv. Landsberg erecta, cv. Li-8, and cv. Lisse, MEDLINE-99126449; PubMed-9927474;
   SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
   Shimura Y.;
   "Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Brassicales; Brassicaceae; Arabidopsis.
  STRAIN=cv. Landsberg erecta;
MEDLINE=95036018; PubMed=7948893;
Okamoto H., Yano A., Shiraishi H., Okada K.,
  Antirrhinum majus.";
Plant Mol. Biol. 26:465-472(1994).
   MEDLINE=92154682; PubMed=1346756;
   Nature 408:820-822(2000).
  SEQUENCE FROM N.A. STRAIN=cv. Columbia;
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
           NCBI_TaxID=3702;
  Brover V., Tr
Feldmann K.;
   thaliana
 eurosids
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  Nature 409:252-529(2001).

-!- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILLARA that is required for autoregulation of both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA or SEPALIARA to form a ternary complex that could be responsible for the requiation of the genes involved in the flower
   STRAIN=cv. Columbia;
MEDLINE=99311297; PubMed=10382288;
Brnnel D., Froger N., Pelletier G.;
"Development of amplified consensus genetic markers (ACGM) in Brassica napus from Arabidopsis thallana sequences of known biological
  KIIZEK B.A., Meyerowitz E.M.;
THE Azabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient
to provide the B class organ identity function.";
Development 122:11-22(1996).
  Riechmann J.L., Krizek B.A., Meyerowitz E.M.; Jahnerization specificity of Arabidopsis MADS domain homeotic proteins APBTALA1, APETALA21, PISTILA47A, and AGAMOUS. "; Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
   Honma T., Goto K.; "Complexes of MADS-box proteins are sufficient to convert leaves into
   SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
   NG M., Yanofsky M.F.; "Activation of the Arabidopsis B class homeotic genes by APETALA1."; Plant Cell 13:739-753(2001).
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length colve (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEO)."; submitted (AGG-2002) to the BMBL/GenBank/DDBJ databases.
  SIMILARITY: Contains 1 K-box dimerization domain.
   EMBL; M86357; AAA32740.1; -.
EMBL; D21125; BAA04665.1; -.
EMBL; AF115798; AAD51887.1; -.
EMBL; AF115799; AAD51888.1; -.
   SEQUENCE OF 36-128 FROM N.A.
   Genome 42:387-402(1999).
  GENETIC REGULATION.
  CHARACTERIZATION.
   CHARACTERIZATION.
  PubMed=11206550;
  development.
   floral organs.";
  PubMed=8565821;
  PubMed=8643482;
   [8]
FUNCTION.
   function.
  PubMed=1
```

```
189 2
851 AA;
  GTPase activation.
DOMAIN 23
  Local Similarity
es 10; Conserv
   NCBI_TaxID=197;
   RPOB_CAMJE
  SEQUENCE
  Query Match
  DOMAIN
   RESULT 12
RPOB_CAMJE
   Best Loca
Matches
   a
   a
ã
  ä
   PROSITE: PS00350; MADS_BOX_1; 1.
PROSITE; PS0066, MADS_BOX_2; 1.
PROSITE; PS50066, MADS_BOX_2; 1.
PROSITE; PS50066, MADS_BOX_2; 1.
DOWALN STANDS-Dinding, Colled coil; Polymorphism.
DOMAIN 93 165 K-BOX.
DOMAIN 75 164 COLLED COIL (POTENTIAL).
VARIANT 31 31 K -> R (in strain cv. Lisse).
  Gaps
   COILED COIL (POTENTIAL).
K -> R (in strain cv. Lisse).
M -> T (in strain cv. Enetagny).
N -> D (in strain cv. Corsacalla-1).
T -> S (in strain cv. Li-8).
L -> V (in strain cv. Kas-1).
E -> K (in strains cv. Chi-1 and cv. Gr-3).
   STRAIN=FVB/N;
MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Mus musculus (Mouse).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  ..
..
  Score 51; DB 1; Length 232;
Pred. No. 2.6;
3; Mismatches 4; Indels
  15-5EP-2003 (Rel. 42, Created)
15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
   851 AA
   107 QRLGECLDELDIQELRRLEDEMENTFK 133
  7 ORYG-----RELRRMSDEFEGSFK 25
   PIR; A42095; A42095.
HSSP; P11746; IMNM.
TRANSFAC, T017767.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; I.
Pfam; PF004185; SRF-TF; I.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; I.
  3;
  34.5%;
   AY070397; AAL49893.1;
AY142590; AAN13159.1;
AF056541; AAD41557.1;
   44.48;
  AAD51894.1;
AAD51895.1;
  CAB81799.1;
AAM64919.1;
               AAD51890.1;
AAD51891.1;
  AAD51897.1;
AAD51898.1;
   AAD51892.1;
  AAD51893.1;
  AAD51896.1;
  AAD51899.1;
   AAD51900.1;
  AAD51901.1;
   AAD51902.1;
  AF115814; AAD51903.1;
  Conservative
   STANDARD;
  165
164
131
47
61
73
109
   Protein C5orf5 homolog
  Query Match
Best Local Similarity
Matches 12; Conserv
   [1]
SEQUENCE FROM N.A.
   NCBI_TaxID=10090;
  AF115805; AF115806; A
             AF115801;
AF115802;
  AF115808;
AF115809;
   93
75
75
61
73
109
  AF115804;
   AF115811;
   AY087369;
   AF115803;
  AF115807;
  AF115810;
  AF115812;
   AF115813;
   CE05_MOUSE
Q8K2H3;
  VARIANT
VARIANT
   VARIANT
   VARIANT
  VARIANT
  CSORF5.
  EMBL;
EMBL;
   EMBL;
EMBL;
EMBL;
   CE05_MOUSE
  EMBL;
  EMBL;
EMBL;
  EMBL;
   EMBL;
   EMBL;
  EMBL;
  EMBL;
   EMBL;
  EMBL;
  MBL;
  EMBL;
  RESULT 11
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DOR NO DO
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Atapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hllyk S.W.,
Athalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
R. "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
   STRAIN-NCTC 11168;
STRAIN-NCTC 11168;
BURDLINE-20150912; Pubmed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
  Gaps
   Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
   046124; 09P131; created)
116-0CT-2001 (Rel. 40, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
  0;
  DB 1; Length 851;
  Indels
   GLU-RICH.
C2B26669FB6DB2CE CRC64;
  .
8
  -!- SIMILARITY: Belongs to the FAM13 family.
  Score 51; DB :
Pred. No. 11;
6; Mismatches
  RHO-GAP
   1 KNLWAAQRYGRELRRMSDEFEGSF 24
  9
   212
256 GLI
97054 MW;
  EMBL; BC031465; AAH31465.1; -. InterPro; IPR000198; RhoGAP.
  34.5%;
41.7%;
  PROSITE; PS50238; RHOGAP; 1.
  Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
  Conservative
  STANDARD;
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NCBI_TaxID=4841;
  RAS3_RHIRA
   SEQUENCE
   Query Match
   RAS3_RHIRA
   Best Loc
Matches
   Mucor
   RESULT 14
   δX
   g
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  2;
  FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
  Gaps
  SEQUENCE FROM N.A.
STRAIN-AICC 15692 / PAO1;
MEDLINE-20437337; Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
  (RNA)(N).
SUBUNIT: THE ENZIME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
   NDLANGVDAA -> MTWLMALMQP (IN REF. 2).
A -> R (IN REF. 2).
C -> S (IN REF. 2).
A -> R (IN REF. 2).
  Calva E.,
"Identification of Campylobacter jejuni and C.coli using the rpoB
gene and a cryptic DNA fragment from C.jejuni.";
Gene 165:1-8(1995).
   CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
   SIMILARITY: Belongs to the RNA polymerase beta chain family.
  . 6
   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                   SEQUENCE OF 338-1031 FROM N.A.
MEDLINE-96084944; PubMed=7489896;
Bustamante V.H., Puente J.L., Sanchez-Lopez F., Bobadilla M.,
  Score 50; DB 1; Length 1378; Pred. No. 25; 3; Mismatches 10; Indels
   DiterPro; IPR001572; RNA_pol_B.
Pfam: PF04563; RNR_pol_Rpb2_1; 1.
Pfam: PF04565; RNR_pol_Rpb2_2; 1.
Pfam: PF04565; RNR_pol_Rpb2_3; 1.
Pfam: PF04565; RNR_pol_Rpb2_3; 1.
Pfam: PF04560; RNR_pol_Rpb2_6; 1.
Pfam: PF04560; RNR_pol_Rpb2_7; 1.
PROSITE: PS01166; RNA_pol_Rpb2_7; 1.
Transferase: Transcription: DNR-directed RNR polymerase;
   )1 A -> R (IN REF. 2).
155915 MW; AB7467C305028EB5 CRC64;
  1306 VWALEAYGAAHTLREMLTIKSDDVEGRFSAYK 1337
   (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
   3 LWAAQRYG--RELRRM----SDEFEGSFKGLK 28
   453 AA
  DNA recombination protein rmuC homolog. RMUC OR PA1031.
   PRT;
   EMBL; X77304; CAB55116.1; -.
   Pseudomonadaceae; Pseudomonas.
  33.8%;
  13; Conservative
   STANDARD;
   Pseudomonas aeruginosa.
   558
671
691
  PIR; A81393; A81393.
PIR; S41868; S41868.
HSSP; Q9KWU7; 1HQM.
   1378 AA;
  Complete proteome.
  Best Local Similarity
  BETA' CHAIN.
   NCBI_TaxID=287;
   SUBSTRATES
  - ! - FUNCTION:
   28-FEB-2003
  28-FEB-2003
   28-FEB-2003
   RMUC_PSEAE
   CONFLICT
  Query Match
  CONFLICT
   CONFLICT
   CONFLICT
  Matches
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   HAD DE PORTE
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   ..
H
   GDP
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
   Gaps
  STRAIN=ATCC 1216B;
MEDLINE=91061774; PubMed=1701021;
MEDLINE=91061774; PubMed=1701021;
MEDLINE=91061774; PubMed=1701021;
MEDLINE=9106174; PubMed=1701021;
Med. Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
Which exhibits striking similarity to human ras genes.",
Mol. Call. Biol. 10:6654-6663(1990).

-!- BNZIME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GIT WICLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GUANINE
NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GIPASE-
ACTIVATING PROTEIN (GAP).
  :- SIMILARITY: BELONGS TO THE SMALL GIPASE SUPERFAMILY. RAS FAMILY.
   Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
Eukaryota, Fungi; Zygomycota, Zygomycetes, Mucorales; Mucoraceae;
   -1- SUBCELLULAR LOCATION: Plasma membrane.
   ,
,
   opportunistic pathogen.";
Nature 406:959-964(2000).
-!- FUNCTION: Involved in DNA recombination (By similarity).
-!- SIMILARITY: BELONGS TO THE RMUC FAMILY.
  DB 1; Length 453;
   Indels
   1E7EA97E82EC5E4B CRC64;
  COIL (POTENTIAL)
  PIR; B83517; E03517.

InterPro; IPR003798; DUF195.

Pfam; PF02646; RmuC; 1.

DNA recombination; Coiled coil; Complete proteome.

Coiled Coil. (POTENUE)

201 COILED COIL (POTENUE)
  01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
   205 AA
   Mismatches
  Score 49; DB
Pred. No. 11;
   PRT;
  4 WAAQRYGR--ELRRMSDE 19
   65 WASERQGREEELRRLASE 82
  EMBL; AE004535; AAG04420.1; -.
  33.1%;
  55.6%;
  Local Similarity 55.6
wes 10; Conservative
   STANDARD;
  GERMLING AND YEAST
  Ras-like protein 3.
   SEQUENCE FROM N.A.
```

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   ó
  phospho-D-gluconate.
--- PARHWAY: Pentose phosphate pathway; second step.
--- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY: 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
   Gaps
   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBL_TaxID=2336;
   -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0
   ;
  GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
BFFECTOR REGION (PROBABLE).
FARNEST, (BY SIMILARITY).
W; DBF086466F090F50 CRC64;
   DB 1; Length 205;
6.3;
  -! - FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6FGL)
FGL OR DEVB OR TM1154.
   PRT; 220 AA.
   Mismatches
  w
w
   Score 48;
Pred. No. 6
   GTP-binding; Prenylation; Lipoprotein.
   InterPro; IPR003577; GIPase_Ras.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
  InterPro; IPR006148; Gluc_gal_isom.
   PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00173; RAS; 1.
TIGRFAMS; TIGRE0031; small_GTP; 1.
  2;
   EMBL; AE001772; AAD36230.1; -.
PIR; F72289; F72289.
  205 AA; 23408 MW;
  32.4%;
62.5%;
   11 RELRRASDEFEGSFKG 26
           EMBL; M55177; AAA83379.1; -.
   Query Match
Best Local Similarity 62.5
Matches 10; Conservative
   STANDARD;
   23
67
125
46
202
                        PIR; C36365; C36365.
  Thermotoga maritima.
   16
63
122
38
202
   TIGE; TM1154;
   6PGL_THEMA
  SEQUENCE
   NP_BIND
NP_BIND
   NP_BIND
  DOMAIN
  09X0N8
   RESULT 15
6PGL_THEMA
  LIPID
  g
  ã
```

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Gaps
  0;
  32.4%; Score 48; DB 1; Length 220; 34.8%; Pred. No. 6.8;
  7; Indels
   proteome.
25325 MW; 9B0FD07EE01E60C3 CRC64;
  Mismatches
   5 AAQRYGRELRRMSDEFEGSFKGL 27
InterPro; IPR005900; Phosphoglucon)
Pfam; PF01182; Glucosamine_iso: 1.
TGRPAMS; TGR01198; pgl; 1.
Hydrolase; Complete proteome.
SEQUENCE 220 AA; 25325 MW; 9B01
   .
8
   Query Match
Best Local Similarity 34.89
Matches 8; Conservative
   DR
DR
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IPR005900; Phosphogluconlac.

Search completed: September 15, 2003, 17:23:01 Job time : 6.6 secs

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menziesia p rhododendro

rhododendro ledum palus

rhododendro

062981 06297 047168 06293 06293 06293 047175 08hsp1 Q8hsp1 Q8hsp1 Q8hsp3 Q8hsp3

Scoring table:

Searched:

Database

Perfect score:

Title:

Sequence:

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protein

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rhododendro rhododendro rhododendro rhododendro rhododendro rhododendro rhododendro

rhododendro rhododendro

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08hsn4 rhododendro

9usu8ō Q8hsn5 rhododendro rhododendro rhododendro

062986 062979 047153 047160 Q8hsp4

menziesia m rhododendro rhododendro rhododendro

rhododendro rhododendro

062993 1 047170 3 047174 3 062983 3

```
[1] ____SEQUENCE FROM N.A.

MEDLINE=20373792; PubMed=10917738;

Inohara N., Nunez G.;

"Genes with homology to mammalian apoptosis regulators identified in
  Brachydanio rerio (Zebrafish) (Danio rerio).

Braxyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBL_TaxID=7955;
  Cell Death Differ. 7:509-510(2000).
Cell Death Differ. 7:509-510(2000).
EMBL, AF231017, AAF66962.2; -.
HSSP, Q92934; 1650.
SFIN; 2DP-GENE-000616-1; bad.
SEOUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
  Last sequence update)
Last annotation update)
   Score 91; DB 13;
Pred. No. 2.1e-05;
   AA
  471 AA.
  Mismatches
   ALIGNMENTS
  146
   |||||::||::|||||||: | :|
LWAAKKYGQQLRRMSDEFDKGMKRVK 114
   3 LWAAQRYGRELRRMSDEFEGSFKGLK 28
  PRT;
  Created)
047173
062990
062974
062993
047170
062983
  062981
062977
047168
062988
  062992
047175
  Q8HSP1
Q8HSP0
Q8HSN9
Q8HSN8
Q8HSN7
   Q8HSN6
Q8HSN5
  Q8HSN4
062985
   062986
062979
047153
047160
Q8HSP4
  PRT;
  ·
6
   61.5%;
ilarity 61.5%;
Conservative 6
  01-OCT-2000 (TEMBLEEL 15, 01-DEC-2001 (TEMBLEEL 19, 01-OCT-2002 (TEMBLEEL 22,
 .
.
  PRELIMINARY;
  PRELIMINARY;
Similarity
16;
Query Match
Best Local S
  89
   Q8ZY71
Q8ZY71;
   Q919N2;
  Q919N2
  Best Loc
Matches
  Bad.
   RESULT 2
   RESULT 1
 2919N2
  Q8ZY71
ID Q
  g
  δŽ
  Q919n2 brachydanio
Q8zy71 pyrobaculum
Q8vjs3 mycobacteri
Q10843 mycobacteri
Q8K016 mus musculu
  047148 menziesia c
047149 rhododendro
047171 rhododendro
062982 rhododendro
062975 rhododendro
062978 rhododendro
062978 rhododendro
062978 rhododendro
047155 rhododendro
   September 15, 2003, 17:17:31 ; Search time 30.4 Seconds (without alignments) 237.680 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Description
   830525
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
   28
   830525 seqs, 258052604 residues
   1 KNLWAAQRYGRELRRMSDEFEGSFKGLK
  SUMMARIES
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               using sw model
  Q8ZY71
Q8VJS3
Q10843
Q8K016
O47148
O47171
O47171
O62975
O62975
   BLOSUM62
Gapop 10.0 , Gapext 0.5
  062989
062978
047155
047152
   sp_invertebrate:*
sp_mammal:*
sp_mhc:*
  sp_unclassified:*
  sp_vertebrate:*
  sp_bacteriap:*
sp_archeap:*
  sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
   sp_organelle:*
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
  sp_rvirus:*
  sp_plant:*
sp_rodent:*
  US-09-544-664-55
  DB
   sp_virus:*
  SPTREMBL 23:*
   sp_phage:*
  protein search,
   Length
   Query
  148
```

0;

Gaps ö

Score

Result No.

Q

Length 146; Indels

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IISSUE=Liver;
  STRAIN-H37RV;
  Query Match
   Q8K016
Q8K016;
                                    Q10843
   RESULT 5
             RESULT 4
  08K016
                         010843
   ద
   ð
  ;
0
   0
  SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
   Gaps
  Gaps
   Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and
  Miller J.H.; "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
  Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
   ó
  .,
0
  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae; Mycobacterium.
NCBL_TaxID-1773;
   38.5%; Score 57; DB 17; Length 471; 44.0%; Pred. No. 7;
   35.8%; Score 53; DB 16; Length 196; ilarity 58.8%; Pred. No. 10; Conservative 1; Mismatches 6; Indels
  Indels
   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1; -.
   Pfam: PF02371; Transposase_20; 1.
SEQUENCE 196 AA; 21349 MW; C145A8D836FD9C2D CRC64;
  Hypothetical protein; Complete proteome.
SEQUENCE 471 AA; 52952 MW; 3B1E36E8AEEZEFOA CRC64;
   Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
   Last sequence update)
Last annotation update)
01-MAR-2002 (TIEMBIRE1. 20, Created)
01-MAR-2002 (TIEMBIRE1. 20, Last sequence update)
01-WAR-2003 (TIEMBIRE1. 23, Last annotation update)
Hypothetical protein PAE0922.
  11;
   Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
EMBL; AB009793; AALG3125.1; -.
InterPro: IPR006638; Elp3.
InterPro: IPR000182; GCNSacetyltransf.
  196 AA.
   3; Mismatches
  404 WQHSGMGRELMRLAEEIAGEFGALK 428
  4 WAAQRYGRELRRMSDEFEGSFKGLK 28
   Created)
  InterPro; IPR003346; Transposase_20.
  SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
Pubmed=11792869;
  PRT;
  134 NIWAADRYNRAIARGHD 150
   Pfam; PF00583; Acetyltransf; 1
SMART; SM00729; Elp3; 1.
  2 NLWAAQRYGRELRRMSD 18
   01-MAR-2002 (TrEMBLRel. 20, 01-MAR-2002 (TrEMBLRel. 20, 01-JUN-2002 (TrEMBLrel. 21, IS1607, transposase.
  Query Match
Best Local Similarity 44.000
These 11; Conservative
   Mycobacterium tuberculosis.
   PRELIMINARY;
  Best Local Similarity
Matches 10; Conserv
   NCBI_TaxID=13773;
  TIGR; MT2070;
  Query Match
   PAE0922
   MT2070
  Q8VJS3
   RESULT 3
   Q8VJS3
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ö
   Associated by September 1970; Standard British
  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   0;
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
   35.8%; Score 53; DB 16; Length 223;
  Indels
   Strausberg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
   PROSITE; PS50234; VWFA; 1.
SEQUENCE 946 AA; 105945 MW; 8B17DBA71B85BC5C CRC64;
  Pfam, PF02371; Transposase_20; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 223 AA; 24132 MW; 70456750017FEF37 CRC64;
  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Inter-alpha trypsin inhibitor, heavy chain 2.
  Last sequence update)
Last annotation update)
  946 AA
223 AA
   Pred. No. 12;
1; Mismatches
   EMBL, 274025, CAA98415.1, -.
Tuberculist, Rv2014, -.
InterPro, IPR003346, Transposase_20.
  Created)
  PRT;
PRT;
   165 NLWAADRYNRAIARGHD 181
  2 NLWAAQRYGRELRRMSD 18
  Hypothetical protein Rv2014.
Rv2014 OR MTCY39.03C.
Mycobacterium tuberculosis.
  58.8%;
  EMBL; BC034341; AAH34341.1;
MGD; MGI:96619; Itih2.
  01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2002 (TrEMBLrel. 20,
  InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
  Conservative
  PRELIMINARY;
PRELIMINARY;
  Best Local Similarity
Matches 10; Conserv
   [1]
SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
  NCBI_TaxID=1773;
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Ξ,
                   SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
  ΒY
   Gaps
   Gaps
   INTRONS (BX SIMILARITY).
-!-SIMILARITY)
-!-SIMILARITY WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
EMBL. G01354; ARAB93448.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk_N.
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
   7;
   7;
  Length 506;
  Length 506;
   Indels
   Indels
   8A6353BFC5F4DC85 CRC64;
   0009EA88CD28549F CRC64;
  01-503. (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
   01-001-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
   Ribosomal maturase (Intron maturase) (Maturase K)
  .
%
  DB 8;
  | :||| | :||| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  DB
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   506 AA.
   506 AA
   5; Mismatches
  34;
   5; Mismatches
  Score 52.5;
Pred. No. 34
  Score 52.5;
  Pred. No.
  EMBL; U61332; AAB93753.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
   PRT;
   PRT;
  Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF014824; Matk_N; 1.
MRNA processing; Chloroplast.
SEQUENCE 506 Aa; 60485 MW; 8A6;
  Pfam; PF01348; Intronmaturas; 1.
Pfam; PF01844; Matk.N; 1.
MRNA processing; Chloroplast.
SEQUENCE 506 AA; 60502 MW; 0009
  35.5%;
  35.5%;
37.5%;
  and
  Query Match
Best Local Similarity 37.55
Matches 12; Conservative
  Query Match
Best Local Similarity 37.5
Matches 12; Conservative
  Rhododendron edgeworthii.
   PRELIMINARY;
   PRELIMINARY;
   MATK OR YCF14.
Rhododendron tashiroi,
   SEQUENCE FROM N.A.
  NCBI_TaxID=49162;
  Chloroplast.
   Kron K.A.;
   098890
   063960;
   047171
  RESULT 9
063960
  RESULT 8
   QD
   SWEER DOWN
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   DT DT DT OS
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  -!-SIMILARITY: WITH CORRESPONDING ORF IN OFFIER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHORDRIAL INTRONS.

BMBL: 161331; AAC15442; 1.

Interpro; IPR000846; Matk.N.

Pfan: PP01348; Intron_maturas2; 1.

Pfan: PP01348; Intron_maturas2; 1.
  Gaps
                                       Gaps
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericcideae; Rhodoreae; Rhododendron.
   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Menziesia.
   "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  7;
   ó
   01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K) (Fragment).
   DB 8; Length 505;
Length 946;
                                       12; Indels
  EE5F927AD2E57DE5 CRC64;
   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
  .;
%
 11;
  390 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 421
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   505 AA.
   Score 52.5; DB Pred. No. 34; 5; Mismatches
  506 AA.
Score 53; DB 1
Pred. No. 58;
5; Mismatches
   212 NVWIMEPOGMRFLHVPDTFEGHFQGV 237
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  Created)
  PRT;
  505 AA; 60233 MW;
   mRNA processing; chloroplast.
NON_TER 1 1
SEQUENCE 505 AA; 60233 MW;
35.8%;
34.6%;
   35.5%;
   (TrEMBLrel. 13,
  (TrEMBLrel. 06,
  INTRONS (BY SIMILARITY)
   Query Match
Best Local Similarity 37.55
Matches 12; Conservative
                                       9; Conservative
  PRELIMINARY;
   Rhododendron kiusianum.
  Menziesia ciliicalyx.
  [1]
SEQUENCE FROM N.A.
Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
   NCBI_TaxID=49167;
  NCBI_TaxID=49154;
  01-JUN-1998 (
01-MAY-2000 (
01-OCT-2002 (
   Chloroplast
   Chloroplast
   Kron K.A.;
  Kron K.A.;
  047148;
  047149
                                     Matches
  RESULT 6
   RESULT 7
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-:- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.
   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermacophyta; Nagnollophyta; eudloctyledons; core eudlocts; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBL_TaxID=49628;
   Rhododendron(Ericaceae) based on matk Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
  21DFF700B071B5B8 CRC64;
  Investigation of Sectional Relationships in the Genus
  Last sequence update)
Last annotation update)
  01-OCT-2002 (TrEMBLrel. 22, Last annotation update
Ribosomal maturase (Intron maturase) (Maturase K).
                               | :||| : || | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  506 AA.
   35.5%; Score 52.5; D
37.5%; Pred. No. 34;
ive 5; Mismatches
   EMBL, AB012732; BAA25853.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
   Created)
  PRT;
   Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; MatK_N; 1.
  506 AA; 60449 MW;
  mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60449 MW;
  01-AUG-1998 (TrEMBLrel. 07,
  INTRONS (BY SIMILARITY)
   Best Local Similarity 37.5
Matches 12; Conservative
   PRELIMINARY;
  PRELIMINARY;
   (TrEMBLrel.
  Rhododendron ponticum.
   Rhododendron ovatum.
   NCBI_TaxID=49169;
  01-0CT-2002
   01-AUG-1998
  Chloroplast
  Query Match
  062972
   062975
   RESULT 11
062975
  RESULT 12
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   A TARGAT T.,

TARGAT T.,

J. JPD. BOL. (0.0 (1998).

-! FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMLARITY).

-! FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLASTS,

AND REGIONS (BY SIMLARITY).

-! SIMILARITY: WITH CORRESPONDING ORE IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY

EMBL; ABOLIZY49; BAA25870.1; -.

EMBL; ABOLIZY45; BAA25866.1; -.

INTERPO: IFROGO842; Intronmaturse2.

InterPro: IFROGO842; Intronmaturse2.

InterPro: IFROGO842; Intronmaturse2.

InterPro: IPROGO842; Intronmaturse2.

InterPro: ARCHAN INTRONMATURE S. 1.

Pfam: PFOL1848; Intronmaturse2; 1.

Pfam: PFOL1848; Intronmaturse2; 1.

Pfam: PFOL1848; Intronmaturse2; 1.

Pfam: PROGSSING; Chloroplast.
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  INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRON
  Gaps
  Gaps
  Chloroplast.

Bukaryock; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericcideae; Rhodoreae; Rhododendron. NCBI_TaxID-75577;
                                      Eukaryoca, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermaclophyta, Magnollophyta, eudicotyledons, core eudicots, Asteridae, Ericaceae, Ericoceae, Ericoceae, Rhodoreae, Rhododendron, NCBL_TAXID=75582, 75580,
  Rhododendron(Ericaceae) based on matk Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
   7;
  ..
  SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
  Length 506;
   DB 8; Length 506;
   [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
  Indels
  Indels
   EMBL, AB012739; BAA25860.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK.N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK.N.; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60419 MW; IF95132CCF4F6B40 CRC64;
  506 AA; 60389 MW; DE0C07AEE608B787 CRC64;
   01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
   Ribosomal maturase (Intron maturase) (Maturase K).
   ä
  .;
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  DB 8;
   | :||| :||| 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
   Score 52.5; DB Pred. No. 34; 5; Mismatches
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  506 AA.
   35.5%; Score 52.5; D
37.5%; Pred. No. 34;
tive 5; Mismatches
  Created)
  PRT;
   35.5%;
  (TrEMBLrel. 07,
   Query Match 35.5
Best Local Similarity 37.5
Matches 12; Conservative
   Conservative
  PRELIMINARY;
   Rhododendron nipponicum.
Rhododendron farrerae.
   Query Match
Best Local Similarity
Matches 12; Conserv
   -AUG-1998
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SEQUENCE

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Gaps

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Indels

8;

DB 8; Length 506;

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Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   Rhododendron(Ericaceae) based on matk Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
   [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
  "Investigation of Sectional Relationships in the Genus
   01-bVG-1998 (TrEMBLrel. 07, Created)
01-bVG-1998 (TrEMBLrel. 07, Last sequence update)
01-cVT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
   506 AA.
  INTRONS (BY SIMILARITY).
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Rhododendron canadense.
  Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
  Chloroplast.
   Query Match
   047155
  047155;
  Matches
  Matches
  RESULT 15
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   INTRONS (BY SIMILARITY).

-!-SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRON
  BY
  Gaps
  Gaps
-:- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.
   Lutaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  7;
  7;
  Length 506;
  DB 8; Length 506;
   SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.
  Indels
  Indels
  Pfam; PF01348; Intron maturas2; 1.
Pfam; PP01824; Matk_N; 1.
PRNA, processin; Chloroplast.
SEQUENCE 506 AA; 60493 NW; D230E54B8C20FEF0 CRC64;
   "Investigation of Sectional Relationships in the Genus Rhododendron(Ericaceae) based on matK Sequences.";
  mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60489 MW; 6D38AlD4D6FEC9BF CRC64;
  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
MATK.
  01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
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  DB 8;
  | :||| | :|| | :|| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  1 KNLWAA----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   506 AA.
   506 AA.
  35.5%; Score 52.5; D
37.5%; Pred. No. 34;
tive 5; Mismatches
  35.5%; Score 52.5; I 37.5%; Pred. No. 34; tive 5; Mismatches
  EMBL, AB012747; BAA25868.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR012866; MatK_N.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; N.
  EMBL, AE012729; BAA25850.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
   Created)
   PRT;
   PRT;
   07,
22,
  12; Conservative
  12; Conservative
   PRELIMINARY;
   PRELIMINARY;
   (TrEMBLrel.
  01-AUG-1998 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel.
   Rhododendron indicum
   Query Match
Best Local Similarity
  Query Match
Best Local Similarity
   NCBI_TaxID=75581;
   01-AUG-1998
  Chloroplast.
  Yukawa T.;
   062978
   062989
  RESULT 13
062989
  Matches
  Matches
  RESULT 14
  062978
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1;
  INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL: U61338; AAR993751.1; -.
Interpro; IPR002442; Intron_maturse2.
Interpro; IRR002866; Matk_N.
   ΒŸ
  Gaps
  Gaps
        Spermātophyta; Magnollophyta; endicotyledons; core endicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
NCBL_TaxID-49465;
   Bukaryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericcideae; Rhodoreae; Rhododendron.NCBL_TaxID=49165;
  INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Rhododendron(Ericaceae) based on matK Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
   "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  7;
  7;
   [1] SEQUENCE FROM N.A. Sobayashi N., Handa T., Takayanagi K., Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K., Yukawa T., Takayanagi K., Yukawa T., Takayana Relationships in the Genus
  8; Length 506;
  8; Length 506;
  Indels
  Indels
   Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60406 MW; 4B5C675CE32218D8 CRC64;
   60350 MW; 5E832589ED64EA25 CRC64;
   01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
   ώ
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  8;
  | :||| :||| | :||| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  DB
   DB
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  506 AA.
  35.5%; Score 52.5; D
37.5%; Pred. No. 34;
Live 5; Mismatches
  5; Mismatches
   Score 52.5;
Pred. No. 34
   EMBL; AB012735; BAA25856.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
  Created)
   PRT;
   Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_W; 1. mRNA_processing; Chloroplar. SEQUENCE 506 AA; 60350 MW; 5E8
  35.5%;
37.5%;
  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
  Rhododendron hongkongense.
  Local Similarity 37.5
les 12; Conservative
  12; Conservative
  PRELIMINARY;
```

391 KPVWAALSDSDIIBRFGRIYRNLSHYYSGSLK 422

Search completed: September 15, 2003, 17:25:50 Job time : 31.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein - protein search, using sw model

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September 15, 2003, 17:16:01; Search time 38.1857 Seconds Run on:

(without alignments) 112.231 Million cell updates/sec

US-09-544-664-56 Title:

143 1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27) Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 segs, 158726573 residues Searched: 1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDE1/goddata/geneseq/geneseqp-emb1/AA1999.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1990.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1991.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1991.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1991.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1991.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1994.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1994.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1995.DAT:\*
| SIDE1/goddata/geneseq/geneseqp-emb1/AA1995.DAT:\*
| SIDE1/goddata/geneseq-geneseqp-emb1/AA1995.DAT:\*
| SIDE1/goddata/geneseq-geneseqp-emb1/AA1995.DAT:\* /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DBT:\*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*
/SIDSI/gcgdata/geneseqg/geneseqp-embl/AA2001.DAT:\*
/SIDSI/gcgdata/geneseqg/geneseqp-embl/AA2002.DAT:\*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\* /SIDSI/goddata/geneseq/geneseqp-embl/AA1982.DAT:\*
/SIDSI/goddata/geneseq/geneseqp-embl/AA1983.DAT:\*
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/SIDSI/goddata/geneseq/geneseqp-embl/AA1986.DAT:\*
/SIDSI/goddata/geneseq/geneseqp-embl/AA1987.DAT:\* A\_Geneseq\_19Jun03:\*
.: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*
:: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                   | 37056 BC12 polypeptide B |       |      |      |      |      | AAR95168 bcl-x(L)/bcl-2 |      |   |
|-------------------------------|--------------------------|-------|------|------|------|------|-------------------------|------|---|
| a                             |                          |       |      |      |      |      |                         |      |   |
| DB                            | .2                       |       | 21   |      |      |      |                         | 19   |   |
| %<br>Query<br>Match Length DB | 3                        | 28    | 26   | 26   | 27   | 162  | 204                     | 204  | • |
| %<br>Query<br>Match           | 100.0                    | 100.0 | 96.5 | 96.5 | 96.5 | 96.5 | 96.5                    | 96.5 |   |
| Score                         | 143                      | 143   | 138  | 138  | 138  | 138  | 138                     | 138  | 0 |
| Result<br>No.                 | 1                        | 7     | M    | 4    | ĸ    | ø    | 7                       | œ    | • |
| ag d                          | 5                        |       |      | . 5. | Ð    |      |                         |      |   |

| Mutant BCL-XL/BCL- | t BCL-   | Murine BAD protein | r murì   | Murine BAD protein | Bad-DTTR apoptosis | Human Bad peptide | PTPC-interacting T | Mutant Bc12 compet | Mutant Bc12 compet | Human Bad peptide |            | BBC6 protein for r | _4  | Human cell prolife |          | Bad p    | acid     | BAD pro | ovari     | $\sim$ | 금        | ad p     | Bcl;     | 7        | 73       | ಗ        | Bad      | Mutant Bc12 compet | Mutant Bcl2 compet | ซ   | Human Bad peptide | ad       | Bad | $\circ$  | Human Bad peptide |
|--------------------|----------|--------------------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|------------|--------------------|-----|--------------------|----------|----------|----------|---------|-----------|--------|----------|----------|----------|----------|----------|----------|----------|--------------------|--------------------|-----|-------------------|----------|-----|----------|-------------------|
| AAW61317           | AAW61318 | AAW58832           | AAB70369 | ABR39082           | 2                  | AAU78627          | 5                  | ABG78484           | 349                | 361               | $^{\circ}$ | AAW32476           | ~   | -1                 | AAB70368 | AAB48287 | AAG67688 |         | ABP41.630 | 0      | ABG78490 | AAU78617 | $\infty$ | $\infty$ | AAU78615 | AAU78616 | AAU78628 | 34                 | 349                | 349 |                   | $\alpha$ | 62  | ABG78485 | 361               |
| 13                 | 13       | 73                 | 22       | 24                 | 22                 | 23                | 23                 | 23                 | 23                 | 23                | 23         | 18                 | 19  | 21                 | 22       | 22       | 22       | 24      | 23        | 17     | 23       | 23       | 23       | 23       | 23       | 23       | 23       | 23                 | 23                 | 23  | 23                | 23       | 23  | 23       | 23                |
| 204                | 204      | 204                | 204      | 204                | 267                | 24                | 25                 | 25                 | 25                 | 25                | 25         | 166                | 168 | 168                | 168      | 168      | 168      | 168     | 201       | 23     | 25       | 25       | 25       | 25       | 25       | 25       | 23       | 25                 | 25                 | 25  | 25                | 25       | 25  | 25       | 25                |
|                    | 96.5     | :                  |          | ٠.                 | ٠.                 | ~                 | ~                  | α.                 | ~                  | ω.                | φ.         | α.                 | α.  | ς.                 | ď.       | cn.      | ς.       | ď.      | ď         | ω.     | ζ.       | ۲,       | 'n.      | w.       | 'n.      | 'n.      | ů.       | Ġ.                 | Ġ.                 | ů.  | v.                | Ġ.       | Ġ.  | 'n.      |                   |
| 138                | 138      | 138                | 138      | 138                | 138                | 114               | 114                | 114                | 114                | 114               | 114        | 114                | 114 | 114                | 114      | 114      | 114      | 114     | 114       | 113    | 111      | 111      | 110      | 110      | 110      | 110      | 109      | 109                | 109                | 109 | 109               | 109      | 109 | 108      | 108               |
| 10                 | 11       | 12                 | 13       | 14                 | 15                 | 16                | 17                 | 18                 | 19                 | 20                | 21         | 22                 | 23  | 24                 | 25       | 26       | 27       | 28      | 29        | 30     | 31       | 32       | 33       | 34       | 35       | 36       | 37       | 38                 | 39                 | 40  | 41                | 42       | 43  | 44       | 45                |

## ALIGNMENTS

Bcl2 polypeptide BH3 domain peptidė #56. AAB37056 standard; peptide; 27 AA. (first entry) 28-FEB-2001 AAB37056; RESULT 1 

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphona/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma, melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

Homo sapiens

WO200059526-A1.

12-OCT-2000.

06-APR-2000; 2000WO-US09352. 99US-0128202. 07-APR-1999;

(UYJE-) UNIV JEFFERSON THOMAS.

rn 2; Huang Z, Wang J, Zhang Z, Shan S,

WPI; 2000-679325/66.

```
The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where to the N-terminus of the peptide where the side chain of the peptide where the side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, where the side chain functional group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides conjugate is a BC1-2 superfamily polypeptide corresponding to a mino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell; lymphoma/leukemia 2 (BC1-2) "mediated blockage of apoptosis in cancer characterized by cancer cells that subject afflicted with a cancer characterized by cancer cells that subject afflicted with a cancer characterized by cancer cells that cancer chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders, acquired conjugate is also useful for treating disorders characterized by monoulymphate is also useful for treating disorders characterized by infarction.

Conjugate is also useful for treating disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   0;
   Gaps
   Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                 New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
   0;
   100.0%; Score 143; DB 21; Length 27; 100.0%; Pred. No. 7.3e-15; ive 0; Mismatches 0; Indels
  Bcl2 polypeptide BH3 domain peptide #55.
   1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
   KNLWAAQRYGRELRRMSDEFEGSFKGL 27
   AAB37055 standard; peptide; 28 AA.
  Claim 18; Page 19; 74pp; English
   (UYJE-) UNIV JEFFERSON THOMAS
  06-APR-2000; 2000WO-US09352.
   99US-0128202.
  28-FEB-2001 (first entry)
   1 Similarity 100.
27; Conservative
   27 AA;
  WO200059526-A1
   Homo sapiens
   07-APR-1999;
   12-OCT-2000.
   Seguence
   Query Match
Best Local S
   AAB37055;
   Matches
   RESULT 2
  ā
   g
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The invention relates to a peptide conjugate having the formula:

(R-X)n peptide where n = 1-10; X = C=0, when the R-X group is attached to the Verminus of the peptide, or a side chain of the peptide where to the University of the peptide, or a side chain is NH2 or NH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is COHH; or alkoxy, 2-14C alkylenyl containing one or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally proup, or benzyl. The peptides Aba37001-B3708 represent examples or two double portion of the conjugate. The peptides chain alkyl group, alkyl group, or benzyl. The peptides Aba37001-B3708 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides conjugate is a Bol-2 superfamily polypeptide corresponding to amino acids 7-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is reversing B cell lumphona/leukemia 2 (Bel-2)-mediated blooky or for reversing B cell lumphona/leukemia (Bloot) in hibiting Bol-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells the express Bol-2. The cancer characterized by cancer cells the express Bol-2. The cancer includes prostate, colorectal, gastic, consumpting the salso useful for treating disorders conjugate is also useful for treating disorders conjugate is also useful for treating disorders conjugate is acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
  ó
  Gaps
   Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bol-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
   or for inhibiting
  cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  0
  Length 28;
  Indels
  100.0%; Score 143; DB 21;
ilarity 100.0%; Pred. No. 7.6e-15;
Conservative 0; Mismatches 0;
   apoptosis
:2
  Ľ
  27
   Bcl2 polypeptide BH3 domain peptide #1.
   peptide conjugates for modulating
   1 KNLWAAQRYGRELRRMSDEFEGSFKGL
  Shan
  AA.
  Claim 18; Page 19; 74pp; English.
  AAB37001 standard; peptide; 26
  stroke; myocardial infarction.
   06-APR-2000; 2000WO-US09352.
  07-APR-1999; 99US-0128202.
  Zhang Z,
  (first entry)
                                       WPI; 2000-679325/66
   Local Similarity
Les 27; Conserv
  Wang J,
   28 AA;
   WO200059526-A1.
   Homo sapiens.
  28-FEB-2001
   12-ocr-2000.
  AAB37001;
   Sequence
  Ζ,
   Query Match
    Huang
  Best Loca
Matches
  RESULT 3
   AAB37001
  29
  qq
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m

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WO200059526-A1
  Sequence
  AAB37003;
   Huang Z,
   Query Match
  Best Loc
Matches
  RESULT 5
   AAB37003
Qγ
  Q
  The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C-0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where to the C-terminus of the peptide, or a side chain of the peptide where the functional group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or conveniented where the side chain functional group is COOH or two double bonds, cyclobutyl, cyclopertyl, cyclobertyl, cyclob
  0;
  Gaps
   m
   Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bc1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/Jeukemia 2, cancer, prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
   New peptide conjugates for modulating apoptosis or for inhibiting
   cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  0;
   Length 26;
  0; Indels
   Score 138; DB 21;
Pred. No.-4.1e-14;
   7
   90.00,
100.0%; Preq. ...
   Ľ
  Bcl2 polypeptide BH3 domain peptide #2.
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   Shan S,
   AAB37002 standard; peptide; 26 AA.
   Claim 18; Page 17; 74pp; English.
   stroke; myocardial infarction.
               (UYJE-) UNIV JEFFERSON THOMAS.
   Zhang Z,
  Query Match
Best Local Similarity 100.0
   (first entry)
  WPI; 2000-679325/66
   Wang J,
  26 AA;
   WO200059526-A1
   28-FEB-2001
  Homo sapiens
   12-OCT-2000
  Sequence
  AAB37002;
  Huang Z,
  RESULT 4
```

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C-0, when the R-X group is attached to the Netranius of the peptide, or a side chain of the peptide where to the Netranius of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or COONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/Leukemia 2 (Bcl-2) mediated blockage of apoptosis in cancer cells: It is also useful for inhibiting a cancer cells: It is also useful for inhibiting a subject as subject and subject afflicted with a cancer characterized by cancer cells that
   express Bol-2. The cancer includes prostate, colorectal, gastric, one-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic lumphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
   Gaps
   Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis medulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma: melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
  New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   ;
0
   96.5%; Score 138; DB 21; Length 26; 100.0%; Pred. No. 4.1e-14;
   Indels
   .;
0
  Lu Z;
   Mismatches
   Bcl2 polypeptide BH3 domain peptide #3.
   27
   26
  Shan S,
   2 NLWAAQRYGRELRRMSDEFEGSFKGL
  AAB37003 standard; peptide; 27 AA.
   100.08;
   Claim 18; Page 17; 74pp; English.
  (UYJE-) UNIV JEFFERSON THOMAS.
   stroke; myocardial infarction.
  Wang J, Zhang Z,
  99US-0128202,
06-APR-2000; 2000WO-US09352.
   (first entry)
   Conservative
  WPI; 2000-679325/66
  Local Similarity
les 26; Conserv
   26 AA;
   Homo sapiens.
  07-APR-1999;
   28-FEB-2001
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0;
  express BC1-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; noctropic; antiiscahemnic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunosuppressive; apoptosis incurdegenerative disease; viral infection; ischaemic cell death; arthritis; infertility; lymphoproliferative condition; inflammation; authritis; infertility;
   Gaps
  New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  0;
  Score 138; DB 21; Length 27;
  Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
  Indels
  .;
0
  4.3e-14;
  Lu Z;
  100.0%; Pred. No. 4.3 ive 0; Mismatches
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  NLWAAQRYGRELRRMSDEFEGSFKGL 26
  Huang Z, Wang J, Zhang Z, Shan S,
   AAB70370 standard; protein; 162 AA.
  Claim 18; Page 17; 74pp; English.
   (UYJE-) UNIV JEFFERSON THOMAS
   96.5%;
                                     06-APR-2000; 2000WO-US09352.
   99US-0128202
   (first entry)
  Local Similarity 100.
Les 26; Conservative
   WPI; 2000-679325/66.
  27 AA;
   07-APR-1999;
   02-MAX-2001
          12-0CT-2000
  AAB70370;
   Sequence
  Query Match
   Best Loc
Matches
   RESULT 6
  AAB70370
  δ
   g
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(i) comprising a less than full length amino acid sequence of a mutant fragment, which contains amino acid substitutions at Serial of a mutant fragment, which contains amino acid substitutions at Serial of a mutant BAD, Serias of a mutane BAD, or Serias of a mutane BAD, (I) has immunostimulant, neuroprotective, notropic, antistement, vulnerary, cytostatic, antivital, antisinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polyucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autolimmune diseases. The present sequence from the present
  ó
  Epitope, murine; bcl-x(L)/bcl-2 associated death promoter; Bad, stroke, polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
  New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13.
  Gaps
  The present invention describes an isolated or synthetic polypeptide
  0
  Length 162;
  neurodegenerative disease; senescence; ischaemia; neoplasia.
  Indels
  bcl-x(L)/bcl-2 associated death promoter protein.
  0
  96.5%; Score 138; DB 22; 100.0%; Pred. No. 3.1e-13;
  100.0%; Pred. ...
  98 NLWAAORYGRELRRMSDEFEGSFKGL 123
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  Claim 7; Page 148-149; 157pp; English.
  AAR95168 standard; Protein; 204 AA.
  (APOP-) APOPTOSIS TECHNOLOGY INC.
  30-MAY-2000; 2000WO-US11864
  99US-0136783
  (first entry)
  Local Similarity 100.
mes 26; Conservative
  WPI; 2001-138734/14.
  162 AA;
  WO200110888-A1
                    Mus musculus.
  06-JAN-1997
  Mus musculus
  28-MAY-1999;
  15-FEB-2001
                                    Synthetic.
  invention
  Sequence
  AAR95168;
  Query Match
  Zhou X;
  Matches
  RESULT 7
  AAR95168
QΣ
  q
```

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WO9817682-A1,
 WO9817682-A1
  AAW61316;
  Sequence
   Query Match
Best Local S
   Matches
   RESULT 9
AAW61316
  δğ
  g
   g
 This sequence represents the murine bcl-x(L)/bcl-2 associated death bcl-x bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and requiates cell death. It has bemology to the bcl-2-related family clustered in the Bill and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of Dcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), but is much less effective at accelerate apoptoric cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-2 or bcl-x(L). Bad competes with Bax for binding to bcl-2 or bcl-x(L) form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
   0
  Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
   Gaps
  Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers
   ;
0
   96.5%; Score 138; DB 17; Length 204; 100.0%; Pred. No. 4e-13;
   0; Indels
  Murine BCL-XL/BCL-2 associated cell death regulator.
                           /note= "BH1 conserved amino acids"
191..192
  /note= "BH2 conserved amino acids"
  100.0%; Prec. ...
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   /note= "PEST sequence"
  /note= "PEST sequence"
   e.g. AIDS, senescence or ischaemia.
Location/Qualifiers
  AAW61315 standard; Protein; 204 AA.
   Claim 3; Fig 1; 130pp; English
   95WO-US14246.
  94US-0333565
  (first entry)
   26; Conservative
  111..130
   (UNIW ) UNIV WASHINGTON
  ..61
   WPI; 1996-251465/25.
N-PSDB; AAT29479.
  Query Match
Best Local Similarity
Matches 26; Conserv
   204 AA;
  Korsmeyer SJ;
  31-OCT-1994;
  07-0CT-1998
   31-OCT-1995;
  WO9613614-A1
   09-MAY-1996.
  AAW61315;
   Seguence
  Mus sp
 Key
Region
  Region
   Domain
  Domain
  RESULT 8
AAW61315
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cath regulator) proteins, having an amino acid other than Ser at ceath regulator) proteins, having an amino acid other than Ser at costition 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein also decrease cell viability, (2) thoreases intracellular delivery. Mutant BAD proteins are used to treat increases intracellular delivery, Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infalmmation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatese. Inhibitors are potentially useful in treatment of excessive apoptosis such as ALDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is defined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have phosphorylated ban, by usual immunoassays. Mutant BAD proteins have phosphorylated on the specified Ser, forming a product that does not proteins in the cytosol, thus promoting cell survival. The mutants with CS ser substituted cannot bind 14-3-3.
   Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
   The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
   Gaps
   New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
   .
0
   96.5%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4e-13; ive 0; Mismatches 0; Indels (
  Mutant BCL-XL/BCL-2 associated cell death regulator #1.
   140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   AAW61316 standard; Protein; 204 AA.
   Claim 1; Fig 10; 95pp; English.
   97WO-US19175.
  96US-0733505.
  (first entry)
  Local Similarity 100.0
   (UNIW ) UNIV WASHINGTON
  WPI; 1998-261422/23.
   204 AA;
  N-PSDB; AAV27833
   Korsmeyer SJ;
  17-0CT-1997;
   18-OCT-1996;
  07-OCT-1998
30-APR-1998
   Mus sp.
Synthetic.
```

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```
Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
   serine substituted mutant; apoptosis; cancer; viral infection.
  Mutant BCL-XL/BCL-2 associated cell death regulator #3.
  140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  AAW61318 standard; Protein; 204 AA.
  07-OCT-1998 (first entry)
  WO9817682-A1
  30-APR-1998.
   Synthetic.
  Seguence
   AAW61318;
   Mus sp
   RESULT 11
AAW61318
П
  δŏ
  The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell catch regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding runant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screen for enhancers and inhibitors of serine-phosphates in the name of serine-phosphates in the name of serine and inhibitors of serine-phosphates. Inhibitors are potentially useful
   Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
  in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
   Gaps
  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
   ;
0
  96.5%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4e-13; Live 0; Mismatches 0; Indels C
  Mutant BCL-XL/BCL-2 associated cell death regulator #2
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  AAW61317 standard; Protein; 204 AA.
  Claim 7; Page 59; 95pp; English.
  96US-0733505.
  97WO-US19175.
   (first entry)
  Best Local Similarity 100.
Matches 26; Conservative
   (UNIW ) UNIV WASHINGTON
  WPI; 1998-261422/23.
  204 AA;
  N-PSDB; AAV27834
   WO9817682-A1
  Korsmeyer SJ;
   07-0CT-1998
  17-0CT-1997;
  18-OCT-1996;
                   30-APR-1998.
   Mus sp.
Synthetic.
  AAW61317;
  Seguence
  Query Match
   RESULT 10
  AAW61317
```

0

Gaps

0

;0

õ

```
The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position ilz and/or 136, relative to the mutant BAD grotein. Also described are: (1) present sequence represents a mutant BAD protein. Also described are: (1) tragments of mutant BAD protein able to decrease cell viability; (2) tragments of mutant BAD protein able to decrease cell viability; (2) thorases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infammation and autoimmune disease. Polymotheotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins animals for use as disease models or in drug screening. BAD creaming as proteins are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, drinibitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, drinibitors dath-promoting activity than wild-type BAD which can become phosphorylated and because the prophorylated on the specified Ser, forming a product that does not betacodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family become broteins in the cytosol, thus promoting cell survival. The mutants with the processive substituted cannot bind 14-3-3.
   New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
  Score 138; DB 19; Length 204;
Pred. No. 4e-13;
0; Mismatches 0; Indels C
   96.5%; Scor
100.0%; Pre
ative 0; 1
   Claim 7; Page 60; 95pp; English.
   97WO-US19175
  96US-0733505.
  Query Match
Best Local Similarity 100.0
Matches 26, Conservative
   (UNIW ) UNIV WASHINGTON
  WPI; 1998-261422/23.
  204 AA;
  N-PSDB; AAV27835
  viral infection
  Korsmeyer SJ;
   17-0CT-1997;
  18-OCT-1996;
30-APR-1998
```

```
WO200110888-A1.
  Mus musculus.
Synthetic.
  28-MAY-1999;
   Korsmeyer SJ;
                                       09-SEP-1997;
  02-MAY-2001
   09-SEP-1996;
   15-FEB-2001
               12-MAR-1998
  Sequence
  AAB70369;
   Query Match
  Matches
   RESULT 13
   AAB70369
  g
 QΫ́
   The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position II2 and/or 136, relative to the murance BAD 914 as sequence. The present sequence represents a mintant BAD protein. Also described are: (1) final proteins of mutant BAD with a heterologous polypeptide that insolo proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lumphoproliferation, arthritis, infertility, concert, inflammation and autoimmune disease. Polywoodie orderengy or to produce transgenic animals for use as disease models or in Guy screening. BAD creating phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in reatment of excessive apoptosis such as AIDS, neurodegeneration, adding activity than wild-type BAD winten become phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD wintch can become phosphorylated on the specified Ser, forming a product that does not beterolimenies with BCL-2 or BCL-XL but instead binds to 14-3-3 family services services in the cytosol, thus promoting cell survival. The mutants with the substituted cannot bind 14-3-3.
   ;
   BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; authormmune diseases.
   Gaps
  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
  0;
  96.5%; Score 138; DB 19; Length 204; 100.0%; Pred. No. 4e-13;
   0; Indels
  100.0%; Pred. ...
   NLWAAQRYGRELRRMSDEFEGSFKGL 165
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   Claim 7; Page 60-61; 95pp; English.
   AAW58832 standard; protein; 204 AA.
            97WO-US19175.
                                      960S-0733505.
   (first entry)
  Conservative
  (UNIW ) UNIV WASHINGTON
   WPI; 1998-261422/23.
N-PSDB; AAV27836.
  Murine BAD protein.
  Best Local Similarity
Matches 26; Conserv
  204 AA;
  viral infection
   Korsmeyer SJ;
            17-0CT-1997;
                                      18-OCT-1996;
  W09809643-A1
  23-JUL-1998
   Sequence
   140
  AAW58832;
   Query Match
   RESULT 12
  AAW58832
   qq
ð
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```
This sequence represents a novel serine-phosphorylated protein, BAD (BOL-XI)RAI-12 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator.

Conformation of a phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphorylated BAD, which act through inhibition/activation of increased/decreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency disease, senescence, neurodegenerative disease, ischaemic cell death, repetiusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Messuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
   ö
   BCI-XL/BCI-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive, apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease, neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death, arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
  Gaps
  Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
   .;
0
   96.5%; Score 138; DB 19; Length 204;
   Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
   Indels
   0;
  Pred. No. 4e-13;
  100.0%; Prec. ...
   140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  AAB70369 standard; protein; 204 AA.
  Claim 3; Fig 8; 61pp; English.
   30-MAY-2000; 2000WO-US11864.
  96US-0707868.
  99US-0136783
97WO-US15871
   (first entry)
   26; Conservative
   (UNIW ) UNIV WASHINGTON.
  WPI; 1998-207049/18.
  Sest Local Similarity
   204 AA;
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us-09-544-664-56.rag

```
204 AA;
  WO200112661-A2.
  16-AUG-1999;
  22-FEB-2001.
  Seguence
   AAU00220;
  Key
Region
   RESULT 15
  ã
   9
  The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amino acid sequence of a mutant and Latel.2 associated cell death requiator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Serl18 of a human BAD, Ser155 of a murine BAD) (1) has immnostimulant, neuroprotective, nocircopic, artisischaemic, vulnearay, cytostatic, antivita, and an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and crivity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis in a cell. Candidate compounds inducing or inhibiting apoptosis, in a cell. Candidate compounds inducing or inhibiting apoptosis, in a cell. Candidate compounds inducing or inhibiting apoptosis, in a cell. Candidate compounds inducing or inhibiting apoptosis, in a cell. Candidate compounds inducing or inhibiting apoptosis, and cell. Candidate compounds inducing or inhibiting apoptosis, in a cell. Candidate compounds inducing or inhibiting assess, neurodegenerative diseases, ischaemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility inflammation and cautolimmume diseases. The present sequence from the present
  0
   Murine; BAD; herpes simplex virus; HSV; US3; herpes virus; apoptosis;
  Gaps
  New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13
  0;
   96.5%; Score 138; DB 22; Length 204; ilarity 100.0%; Pred. No. 4e-13; Conservative 0; Mismatches 0; Indels (
  27
   2 NLWAAQRYGRELRRMSDEFEGSFKGL
   Claim 4; Page 148; 157pp; English.
                    (APOP-) APOPTOSIS TECHNOLOGY INC
  ABR39082 standard; Protein; 204
  Murine BAD protein SEQ ID NO:4.
   31-JUL-2002; 2002WO-US24177.
  31-JUL-2001; 2001US-308929P.
  (first entry)
   Munger J, Roizman B;
   (UYCH-) UNIV CHICAGO
  WPI; 2003-248168/24.
  virucide; infection
   WPI; 2001-138734/14
   Local Similarity
nes 26; Conserv
   204 AA;
  WO2003012049-A2
  10-MAY-2003
   Mus musculus
  13-FEB-2003.
   Sequence
   ABR39082;
   Query Match
  Zhou X;
   Best Loc
Matches
  RESULT 14
   ABR39082
```

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The present invention describes a method (MI) for inducing apoptosis in a cell infected with herpes simplex virus (HSV), which comprises administering to the cell, a composition having an agent that inhibits phosphorylation of pro-apoptotic polypeptide BAD by HSV US3. Also described is a method (M2) for treating a patient infected with HSV, by administering to the patient, a composition comprising a peptide comprising a sequence of 4-100 continuous amino acids sequence (see ABRS90B1), where the peptide comprises seall2, seal13, or ser155, or their combinations. BAD has virucide activity. M is useful for inducing apoptosis in a cell infected with HSV, where the cell is in a human. M2 its useful for treating a patient infected with HSV. The present sequence represents murine BAD, which is used in the exemplification of the present invention.
  Mouse; Bad-DTTR; apoptosis; cancer; spinal muscular atrophy; diphtherata toxin receptor binding domain; DTR; neoplasm; timour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
Inducing apoptosis in a cell infected with herpes simplex virus, {\rm HSV}_{\rm c} by administering to the cell, a composition comprising an agent that inhibits phosphorylation of pro-apoptotic polypeptide {\rm BAD} by {\rm HSV} {\rm US3}
  Gaps
  .
0
  Score 138; DB 24; Length 204; Pred. No. 4e-13;
  0; Indels
   Bad-DTTR apoptosis-modifying fusion protein.
  Mismatches
   /note= "10x histidine tag"
   (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
  140 NLWAAQRYGRELRRMSDEFEGSFKGL 165
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   Corynebacterium diptheriae.
Synthetic.
  Location/Qualifiers
   Claim 15; Page 168; 192pp; English.
   AAU00220 standard; Protein; 567 AA
   96.5%; Scut
100.0%; Pred
0; M
  99US-0149220
  15-AUG-2000; 2000WO-US22293
  Youle RJ, Liu X, Collier
  31-MAY-2001 (first entry)
  Conservative
  Query Match
Best Local Similarity
  Huntington's disease
  WPI; 2001-218343/22.
N-PSDB; AAS00248.
  Chimeric - Mus sp.
Chimeric - Coryneba
Chimeric - Synthet:
```

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Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response of cell
```

Claim 4; Page 59-61; 65pp; English.

The sequence represents the amino acid sequence of Bad-DTTR apoptosismodifying fusion protein comprising Bad gene sequence fused via a short
linker to diphtheria toxin translocation domain (DTTR). The
linker to diphtheria toxin translocation domain (DTTR). The
linker to diphtheria toxin translocation domain (DTTR). The
linker to diphtheria toxin toxin protein is capable of binding a
located cell. The apoptosis-modifying fusion protein comprises at least
crarget cell. The BDTR domain, which targets the fusion protein to the
larget cell. The fusion protein is useful for modifying
cof the target cell. The fusion protein is useful for modifying
(inhibiting or enhancing) apoptosis in a target cell, such as neuron,
lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
hyper-proliferative cell or an adipocyte. It is also useful for reducing
apoptosis in a subject after translent ischaemic neuronal injury,
especially spinal cord injury. The fusion protein may be used to treat
various diseases and injury conditions through inhibition or enhancement
of apoptotic cellular response, including neurodegenerative disorders
such as Alzheimer's disease, Huntington's disease, spinal muscular
catrophy, stroke episodes and unequilated cell growth as in tumours and
atrophy, stroke episodes and unequilated cell growth as in tumours and
effectively throughout the body and targeted to selective tissue and 

567 AA; Seguence

Gaps 0; Query Match 96.5%; Score 138; DB 22; Length 567; Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 26; Conservative 0; Mismatches 0; Indels 0

2 NLWAAQRYGRELRRMSDEFEGSFKGL 27

161 NIWAAQRYGRELRRMSDEFEGSFKGL 186

В

Search completed: September 15, 2003, 17:22:14 Job time: 38.1857 secs

Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 31458, A Sequence 23807, A Sequence 5, Appli Sequence 5, Appli

Sequence 3

Sequence 4, Appli Sequence 17508, A Sequence 28775, A Sequence 27, Appl Sequence 27, Appl Sequence 20, Appl Sequence 20, Appl Sequence 18729, A

Scoring table:

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score:

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protein

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96.5%; Score 138; DB 1; Length 204; 100.0%; Pred. No. 1e-13; 1ive 0; Mismatches 0; Indels
  /note= "Deduced amino acid sequence of mouse BAD."
   Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION
GENERAL INFORMATION: RORSMER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF EQUENCES: 59
CORRESPONDENCE ADDRESS:
   CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000700
TELEPHONE: (415) 326-240
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
US-09-328-352-4656
US-09-252-991A-19594
US-09-088-774-3
US-09-88-774-3
US-09-252-991A-31458
US-09-252-991A-3807
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COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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   single
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COS-333-565-2
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Best Local Similarity
Matches 26; Conserv
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  TOPOLOGY:
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Appli
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   Sequence 26,
   Sequence 13,
Sequence 14,
Sequence 3,
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-661-479-2
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   SUMMARIES
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
  US-09-544-664-56
  Query
Match Length
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Score

Result . ي ó

Gaps

0;

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  SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
  : 168 amino acids
amino acid
   CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
  Query Match
Best Local Similarity 91.73
Matches 22; Conservative
  Ouery Match
Best Local Similarity 91.7
Matches 22; Conservative
  single
  TOPOLOGY: linear MOLECULE TYPE: protein US-08-665-617-2
  MOLECULE TYPE: protein
  linear
   STRANDEDNESS:
   TOPOLOGY:
   US-08-717-123-2
   US-08-717-123-2
  δŻ
   ö
  ..
0
   Gaps
   Gaps
   Gene and Protein for Regulation of Cell Death
  ó
   0;
  94.4%; Score 135; DB 4; Length 204; 96.2%; Pred. No. 2.9e-13; tive 1; Mismatches 0; Indels
   ENCODING NUCLEIC
   Length 204;
   0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
  Score 135; DB 2;
Pred. No. 2.9e-13;
1; Mismatches 0;
  Second Se
   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xudong, Xin
TITLE OF INVENTION: Gene and Protein for Re
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
  140 NIWAAQRYGRELRRWIDEFEGSFKGL 165
  140 NLWAAQRYGRELRRMTDEFEGSFKGL 165
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-6001
TELEFAX: (619) 535-6049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
  US-08-665-617-2; Sequence 2, Application US/08665617; Patent No. 5663316
   94.48;
96.28;
   : 204 amino acids amino acid
  Query Match
Best Local Similarity 96.28
Matches 25; Conservative
  25; Conservative
  FILING DATE:
CLASSIFICATION: 530
  ; ORGANISM: Mus musculus US-09-375-257-3
   STREET: 2421 N.W. CITY: Gainesville STATE: Florida
  Query Match
Best Local Similarity
  COUNTRY: US
   ; TOPOLOGY:
US-08-717-123-3
   SEQ ID NO 3
LENGIH: 204
  RESULT 8
US-09-375-257-3
   LENGIH:
   TYPE: PRT
  Matches
  RESULT 9
   å
   g
  QY
   qq
```

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ö
  ö
  Gaps
   ô
  ·;
   Sequence 2, Application US/08717123
Patent No. 596703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE
  79.7%; Score 114; DB 1; Length 166; 91.7%; Pred. No. 4e-10;
  79.7%; Score 114; DB 2; Length 168; 91.7%; Pred. No. 4e-10;
   2; Indels
  2; Indels
   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
   0; Mismatches
  0; Mismatches
  ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2;
SEQUENCE CHARACTERISTICS:
   101 NIWAAQRYGREIRRMSDEFVDSFK 124
   103 NLWAAQRYGRELRRMSDEFVDSFK 126
  2 NIWAAQRYGRELRRMSDEFEGSFK 25
  2 NLWAAQRYGRELRRMSDEFEGSFK 25
NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 375-8100
INFORMATION FOR SEQ ID NO: 2:
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Query Match 79.7%; Score 114; DB 3; Length 168; Best Local Similarity 91.7%; Pred. No. 4e-10; Matches 22; Conservative 0; Mismatches 2; Indels
  APPLICANT: Hillman, Jennifer L.
APPLICANT: Vue, Henry
APPLICANT: Vue, Henry
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Oorley, Neil C.
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: EBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLENG for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
  CFERKHING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILLING DATE:
  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0421 US
  103 NLWAAORYGRELRRMSDEFYDSFK 126
  2 NLWAAQRYGRELRRMSDEFEGSFK 25
  78-09-410-372-1
; Sequence 1, Application US/09410372
; Patent No. 6281334
  TELEPHONE: 650-855-0555
  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windc
   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
   TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS
   LIBRARY: GenBank
CLONE: 1683637
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   GENERAL INFORMATION:
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   USA
   94304
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COUNTRY:
  TOPOLOGY:
   US-08-985-335-7
   COUNTRY:
  STATE:
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   79.7%; Score 114; DB 3; Length 168; ilarity 91.7%; Pred. No. 4e-10; Conservative 0; Mismatches 2; Indels
   GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tue, Henry
APPLICANT: Lal, preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
ITILE OF INVENTION: PROMEINS ASSOCIATED WITH CELL
ITILE OF INVENTION: PROMEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmacentian
  PROTEINS ASSOCIATED WITH CELL PROLIFERATION
   OPERATING SYSTEM: DOS
SOCHWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAMB: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
RECISTRATION NUMBER: 36,749
RECISTRATION NUMBER: PF-0421 US
TELECHOME: 650-855-0555
TELECHOME: 650-855-0555
   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
  103 NLWAAQRYGRELRRMSDEFVDSFK 126
  2 NIWAAQRYGRELRRMSDEFEGSFK 25
   Sequence 7, Application US/08985335; Patent No. 608084; Patent No. 608084; Patent No. 608084; Patent No. Patent No. Patent No. Patent Napplicany: July, Preeti APPLICANY: Jal, Preeti APPLICANY: Shah, Puryi APPLICANY: Shah, Puryi APPLICANY: Corley, Neil C. TITLE OF INVENTION: PROTEINS ASSOCTITLE OF INVENTION: PROTEINS ASSOCTITUTED
  ; Sequence 1, Application US/08985335; Patent No. 6080847
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STRANDEDNESS: single
; TOPOLOGY: linear
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; CLONE: 358673
US-08-985-335-1
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local Similarity
Matches 22; Conserv
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   94304
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   STATE: C. COUNTRY:
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US-08-985-335-1
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CLONE: 1683637
US-09-410-372-7
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   APPLICANT: Hillman, Jennifer L.
APPLICANT: Tuc, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTERMS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
  CERKATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
APPLICATION NUMBER: 08/985,335
   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
  PF-0421 US
  103 NLWAAQRYGRELRRMSDEFVDSFK 126
  2 NIWAAQRYGRELRRMSDEFEGSFK 25
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FLING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGIGERATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
   Sequence 7, Application US/09410372 Patent No. 6281334
  STATE: CA
COUNTRY: USA
1TP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SISTEM: DOS
  TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
  LENGTH: 168 amino acids TYPE: amino acid
  SEQUENCE CHARACTERISTICS:
  single
   NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
  ; TOPOLOGY: 11near; INMEDIATE SOURCE: : LIBRARY: SYNORAB01 : CLONE: 358673 US-09-410-372-1
   SYNORAB01
  GENERAL INFORMATION:
  STRANDEDNESS:
  US-09-410-372-7
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   Sequence 2, Application US/09375257

Patent No. 6504022

GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: HORNAN BAD POLIPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 460140.42601

CURRENT APPLICATION NUMBER: US/09/375,257

CURRENT PILING DATE: 1999-08-16

NUMBER OF SEQ ID NOS: 15

SOFFWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 2

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Pred. No. 4e-10;
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Best Local Similarity 91.7%;
Matches 22; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

## Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 17, Appli Sequence 147, Appli Sequence 147, Appli Sequence 241, Appli Sequence 241, Appli Sequence 3, Appli Sequence 1, Appli Description 4 US-10-066-179-3 5 US-10-059-261-258 US-09-84-657-1 US-09-84-657-1 US-09-84-657-1 US-09-84-657-1 US-10-05-179-2 US-10-179-2 US-10-179-2 US-10-179-2 US-10-179-2 US-10-178-179-1 US-09-1750-1 US-09-824-1750-2 US-10-092-750-2 US-10-156-761-1154-1 US-09-815-242-3 US-09-815-242-3 US-09-922-378-3 Query Match Length DB Score Result No. 24221098765

| Sequence 8, Appli<br>Sequence 12463, A<br>Sequence 120, Appli<br>Sequence 20, Appli<br>Sequence 18, Appli<br>Sequence 23, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 1881, Appli<br>Sequence 1881, Appli<br>Sequence 1881, Appli<br>Sequence 1881, Appli<br>Sequence 501, Appli | NOCLEIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Length 204;<br>Indels 0; Gaps 0;                      | NUCLEIC                                                                                                                                                                                                                                         |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 14 US-10-008-355-8<br>9 US-09-815-242-12463<br>12 US-10-008-355-2<br>12 US-10-368-245-2<br>13 US-09-881-752A-238<br>14 US-09-881-752A-238<br>15 US-10-166-135-2<br>15 US-10-166-135-2<br>15 US-10-166-135-2<br>15 US-10-166-135-2<br>15 US-10-166-357-2<br>15 US-10-166-357-2<br>15 US-10-166-357-2<br>15 US-10-166-357-2<br>15 US-10-166-357-2<br>15 US-10-166-357-2<br>15 US-10-251-385-198<br>10 US-09-989-722-501<br>10 US-09-989-722-501<br>10 US-09-989-723-501<br>10 US-09-989-723-501                                                                                                                                                                                                                                                                                                                              | ALIGNMENTS 1922378 an DPOLYPEPTIDES, ENCODING ND METHODS OF USE US/09/922,378 18-03 18-03                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 135; DB 9;<br>No. 5.5e-12;<br>matches 0;<br>27<br>165 | on US/10066179 20115631&1 111am A. 117, Tilman POLYPEPTIDES, ENCODING NUCLEIC ACIDS AND METHODS OF USE                                                                                                                                          |
| $\begin{array}{c} 0.00000000000000000000000000000000000$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | RESULT 1  Sequence 3, Application US/099223; Sequence 3, Application US/099223; Petent No. US200203786941  GENERAL INFORMATION: APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: ACIDS AND MI TITLE OF INVENTION: HUMAN BAD POI TITLE OF INVENTION: ACIDS AND MI TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 94.4<br>96.2<br>ative<br>ELRRMS:                      | TESULT 2  35-10-066-179-3  Sequence 3, Application US/10066  Publication No. US20020115631A1  GENERAL INFORMATION:  APPLICANT: HORDE, William A.  APPLICANT: OlterSourf, Tilman  TITLE OF INVENTION: HUMN BAD I.  TITLE OF INVENTION: RUMN BAD. |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Applica<br>Applica<br>RMATION<br>BOTOS.<br>Olters.<br>VENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION<br>WENTION | imilarity<br>; Conserv.<br>NEWAAQRYGR.<br>            | 3 Applice No. US2 RMATION HORDE, Olter VENTION                                                                                                                                                                                                  |
| ቀቁ-ቀቁ-የመለጠ የመጠ የመጠ የመጠ የመጠ የመጠ የመጠ የመጠ የመጠ የመጠ የመ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | UULT 1  90-922-378-3  90-922-378-3  30-922-378-3  30-922-378-3  30-922-378-3  30-922-378-3  30-922-378-3  90-922-378-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | atch<br>3al S<br>25<br>2<br>2                         | 2<br>66-179-<br>nnce 3,<br>cation<br>AL INFO<br>LICANT:<br>LICANT:<br>LICANT:                                                                                                                                                                   |
| 11111222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | RESULT   US-09-97   OS-09-97   OS-097   O                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Query Ma<br>Best Loc<br>Matches<br>Qy<br>Db           | RESULT US-10-0 ; Seque ; Publi ; GENER ; APPL ; APPL                                                                                                                                                                                            |

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Length 168;

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79.7%; Score 114; DB 9; Length 168; 91.7%; Pred. No. 5.1e-09; Live 0; Mismatches 2; Indels
  PPLICANT: Hilling:
Yue, Henry
Lal, Preet;
Shah, Purvi
Corley, Nell C.
TITLE OF INVENTION: PROLIFERATION
PROLIFERATION
   COMPUTER: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/410,372
FILING DATE: CAURNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 95/41 US
REGISTRATION NUMBER: 95/42 US
TELEPOMNUMICATION INFORMATION:
TELEPOMNUMICATION INFORMATION:
TELEPOMS: 650-855-055
TELEPAR: 650-855-04166
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
  Query Match 79.7%; Score 114; DB 9; Best Local Similarity 91.7%; Pred. No. 5.1e-09; Matches 22; Conservative 0; Mismatches 2;
   CLONE: 358673
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
  103 NLWAAQRYGRELRRMSDEFVDSFK 126
   103 NLWAAQRYGRELRRMSDEFVDSFK 126
  2 NIWAAQRYGRELRRMSDEFEGSFK 25
   2 NLWAAQRYGRELRRMSDEFEGSFK 25
   sequence 1, Application US/09894657
patent No. US20020095569A1
centary. INFORMATION:
    APPLICANT: Hillman, Jennifer L.
   LENGIH: 168 amino acids
  TYPE: amino acid
STRANDEDNESS: single
  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
  LIBRARY: SYNORABO1
CLONE: 358673
  COMPUTER READABLE FORM:
  TOPOLOGY: linear
   22; Conservative
  COUNTRY: USA
ZIP: 94304
; ORGANISM: Homo sapiens US-09-922-378-2
  IMMEDIATE SOURCE
   Query Match
Best Local Similarity
Matches 22; Conserv
   STATE: CA
   RESULT 6
US-09-894-657-7
  US-09-894-657-1
   US-09-894-657-I
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  US-10-059-261-258

| Sequence 258, Application US/10059261
| Publication No. US200300778261
| GENERAL INFORMATION:
| APPLICANT: BDELMAN, LENA
| APPLICANT: BDELMAN, LENA
| APPLICANT: BTRIAND, JEAN-PAUL
| TILE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
| TILE OF INVENTION: PUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
| TILE OF INVENTION: (PIPC)
| TILE OF INVENTION: (PIPC)
| TILE OF INVENTION: (PIPC)
| TILE OF INVENTION: (PIPC)
| TILE OF INVENTION: (PIPC)
| TILE OF INVENTION: (PIPC)
| FILE REPERENCE: 03495.0216
| CURRENT APPLICATION NUMBER: (0/265,594)
| PRIOR APPLICATION NUMBER: 60/265,594
| PRIOR APPLICATION NUMBER: 60/265,594
| NUMBER OF EQUIN OF THE PERMEABILITY TRANSITION PORE COMPLEX
| SEQ ID NOS: 325 | | NUMBER: PATENTIN OF THE PERMEABILITY TRANSITION OF THE PERMEABILITY TRANSITION PORE COMPLEX
| TILE REPERENCE: 03495.0216
| CURRENT APPLICATION NUMBER: 60/265,594 | NUMBER: PATENT APPLICATION PORE COMPLEX
| SEQ ID NOS: 325 | | NUMBER OF THE PERMEABILITY TRANSITION OF THE PERMEABILITY TRANSITION OF THE PERMEABILITY TRANSITION OF THE PERMEABILITY TRANSITION OF THE PERMEABILITY TRANSITION PORE COMPLEX
| TILE PERMEABILITY TRANSITION PORE COMPLEX OF THE PERMEABILITY TRANSITION PORE COMPLEX PROPER PROPERTY PRIOR PAPEL CALINO PORE COMPLEX PROPERTY PR
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   ; OTHER INFORMATION: Description of Unknown Organism: TOX peptide US-10-059-261-258
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  94.4%; Score 135; DB 14; Length 204; 96.2%; Pred. No. 5.5e-12;
  Length 25;
   GENERAL INFORMATION:
APPLICANT: HORN-, WALLIAM A.
APPLICANT: HORN-, WALLIAM A.
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERANCE: 480140, 42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
  Indels
  Indels
   Query Match 79.7%; Score 114; DB 15; Best Local Similarity 91.7%; Pred. No. 7.4e-10; Matches 22; Conservative 0; Mismatches 2;
   1; Mismatches
FILE REFERENCE: 480140.428C1
CURRENT APPLICATION NOWBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 204
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  2 NLWAAQRYGRELRRMSDEFEGSFK 25
  1 NIWAAQRYGRELRRMSDEFVDSFK 24
  ; Sequence 2, Application US/09922378
; Patent No. US20020037869A1
   TYPE: PRT
ORGANISM: Unknown Organism
   Query Match
Best Local Similarity 96.23
Matches 25; Conservative
   ; ORGANISM: Mus musculus US-10-066-179-3
   RESULT 4
US-09-922-378-2
  SEQ ID NO 2
LENGIH: 168
  TYPE: PRT
   TYPE: PRT
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us-09-544-664-56.rapb

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STATEMENT CATE THE OWN-TION:
APPLICANT: Call Signaling Technology, Inc.
APPLICANT: Call Signaling Technology, Inc.
APPLICANT: Call Signaling Technology, Inc.
APPLICANT: Call Michael J.
APPLICANT: CALL
TILLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPEC.
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCH:
FILE REPERENCE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US, 10/1/14, 105A
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin Version 3.1
IENGTH: 15
   Sequence 1077, Application US/10238075
Publication No. US20030148324A1
GENERAL INPORMATION:
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are iso TITLE OF INVENTION: E.Cali, and biological uses of these polynucleotides and of t TITLE OF INVENTION: E.Cali, and biological uses of these polynucleotides and of t TITLE OF INVENTION: E.Cali, and biological uses of these polynucleotides and of t CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR RILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1077
   ). LOCATION: (8)...(8) ..., OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
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  Gaps
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0
  Length 168;
   49.7%; Score 71; DB 15; Length 15; 100.0%; Pred. No. 0.0008; tive 0; Mismatches 0; Indels
  Indels
   79.7%; Score 114; DB 14;
91.7%; Pred. No. 5.1e-09;
tive 0; Mismatches 2;
   103 NIWAAQRYGRELRRMSDEFVDSFK 126
  2 NIWAAQRYGRELRRMSDEFEGSFK 25
   Sequence 147, Application US/10174105A; Publication No. US20030068652A1; GENERAL INFORMATION:
   OTHER INFORMATION: Synthetic Peptide
   TYPE: PRT
ORGANISM: Artificial Sequence
  10 GRELRRMSDEFEGS 23
   Query Match
Best Local Similarity 91.79
Matches 22, Conservative
  Query Match
Best Local Similarity 100.
Matches 14; Conservative
  TYPE: PRT
ORGANISM: Escherichia coli
       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-179-2
  NAME/KEY: MOD_RES
  RESULT 8
US-10-174-105A-147
   US-10-238-075-1077
   FEATURE:
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  Gaps
   0;
  US-10-066-179-2

Sequence 2, Application US/10066179

Sequence 2, Application US/10066179

Publication No. US20020115631A1

GENERAL INFORMATION:

APPLICANT: HORNE, William A.

TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND WETHODS OF USE

FILE REFERENCE: 480140.428C1

CURRENT APPLICATION NUMBER: 2002-02-01

NUMBER OF SEQ ID NOS: 15

SOFWMARE: FASTERQ for Windows Version 4.0
   Query Match 79.7%; Score 114; DB 9; Length 168; Best Local Similarity 91.7%; Pred. No. 51e-09; Matches 22; Conservative 0; Mismatches 2; Indels Matches 24; Conservative 0; Mismatches 25; Indels
   PPLICANT: HILLMAN,
Yue, Henry
Lal, Preeti
Shah, Purvi
Corley, Neil C,
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
  COMPUTER: IEM COMPACINE

COMPUTER: IEM COMPACINE

OPERATING SYSTEM: DOS

SOSTWARE: FASLSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/894,657

FILING DATE: 28-Jun-2001

PRIOR APPLICATION NUMBER: 09/410,372

FILING DATE: CUNROWN-

TILING DATE: CUNROWN-

ATTORNEY/AGENT INPORMATION:

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: 36,749

TELEPHONE: 650-865,055

TELEPHONE: 650-865,055

TELEPHONE: 650-865,055
   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Forter Dr. CITY: Palo Alto
  SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-894-657-7
   103 NLWAAQRYGRELRRMSDEFVDSFK 126
  2 NLWAAQRYGRELRRMSDEFEGSFK 25
Sequence 7, Application US/09894657
Patent No. US/20020088569A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
   LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   SEQUENCE CHARACTERISTICS
   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
   IMMEDIATE SOURCE:
LIBRARY: GenBank
  TOPOLOGY: linear
  CLONE: 1683637
  COUNTRY: USA
ZIP: 94304
   STATE: CA
   SEQ ID NO 2
LENGIH: 168
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32.9%; Score 47; DB 15; Length 138; 45.5%; Pred. No. 24;
   US-10-092-750-241

Sequence 241, Application US/10092750

Publication No. US20030032157A1

Publication No. US20030032157A1

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia A.

APPLICANT: Alpin, Martin C.

TITLE OF INPENTION POLYPEPTIGES Interactive with BCL-X1

FILE REFERENCE: 50036/05002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2003-03-07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR FILING DATE: 2003-03-07
   Indels
   Guegler, Karl J.
Patterson, Chandra
TITLE OF INVENTION: ESCOPTATED TRYPSIN-TYPE
INHIBITOR HEAVY CHAIN PRECURSOR
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: WORD PERFECT 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
CLASSIFICATION: <URNOwn>
  NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/COCKET WIMBER: PF-0505 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPRAX: 650-845-4166
  3; Mismatches
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/388,774
FILING DATE: <Unknown>
   NUMBER OF SEQ ID NOS: 253 SOFTWARE: FastSEQ for Windows Version 4.0 \,
  APPLICANT: Hillman, Jennifer L.
   3 LWAAQRYGRELRRMSDEFEGSF 24
   3 LWAAQRYGRELRRMSDEFEGSF 24
  ; Sequence 3, Application US/09828423
; Patent No. US20020099178A1
; GENERAL INFORMATION:
  ATTORNEY/AGENT INFORMATION:
   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   Query Match 32.9
Best Local Similarity 45.5
Matches 10; Conservative
  NUMBER OF SEQUENCES:
  CITY: Palo Alto
  Guegler,
   STATE: CA
COUNTRY: USA
   ; ORGANISM: Homo sapiens
US-10-092-750-241
   SEQ ID NO 241
LENGTH: 138
   US-09-828-423-3
   TYPE: PRT
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  US-10-092-750-1

Sequence 1, Application US/10092750

Publication No. US20030032157A1

Sequence 1, Application No. US20030032157A1

SEMERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Hammond, Philip W.

APPLICANT: Marght, Martin C.

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

FILE REPERENCE: 50036/05002

CURRENT PELING DATE: 103-002-03-07

PRIOR PILING DATE: 2002-03-07

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE FASTERE (FILING DATE: 2001-03-08

SOFTWARE (FILING DATE: 2001-03-08

   35.0%; Score 50; DB 15; Length 215; 56.2%; Pred. No. 14; tive 4; Mismatches 3; Indels
   Query Match
Best Local Similarity 40.7%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 11; Indels
   32.9%; Score 47; DB 15; Length 35; 45.5%; Pred. No. 5.9; tive 3; Mismatches 5; Indels
   RESULT 10

US-10-156-761-9145

Sequence 9145, Application US/10156761

Publication No. US20303199018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI

APPLICANT: ISHIKANA, UNN

APPLICANT: ISHIKANA, UNN

APPLICANT: SHIRANA, HAROO

APPLICANT: HARTORI, WASAHIRA

APPLICANT: HARTORI, WASAHIRA

TITLE OF INFORMATION NOVEL POLICANT

CURRENT PALLING DATE: 2001-05-30

PRIOR PELING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: UF 2001-272697

PRIOR APPLICATION NUMBER: UP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

SEQ ID NO 9145

SEQ ID NO 9145
  1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
   ) ORGANISM: Streptomyces avermitilis US-10-156-761-9145
  :|:| :|||| || :|
ERWGGDLRRMRDEADG 123
   7 ORYGRELRRMSDEFEG 22
   Conservative
  Ouery Match 35.0
Best Local Similarity 56.2
Matches 9; Conservative
  ORGANISM: Homo sapiens
  Best Local Similarity Matches 10; Conserv
   US-10-238-075-1077
  US-10-092-750-1
   LENGIH: 35
  TYPE: PRT
   108
  Query Match
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Gaps

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Query Match 30.8%; Score 44; DB 9; Length 426; Best Local Similarity 36.8%; Pred. No. 2.1e+02; Matches 7; Conservative 4; Mismatches 8; Indels
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-37

PRIOR FILING DATE: 2000-10-37

PRIOR FILING DATE: 2000-10-37

PRIOR PRILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-21

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASLESQ for Windows Version 4.0

LENGTH: 426
   Search completed: September 15, 2003, 17:47:53 Job time: 21.4071 secs
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386 FGGSLRRQDENFDGKIKAI 404
  9 YGRELRRMSDEFEGSFKGL 27
  TYPE: PRT ORGANISM: Staphylococcus aureus US-09-815-242-5704
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  Length 272;
   .core 46; DB 9; Length 946;
pred. No. 2.4e+02;
5; Mismatches 13; Indels
   Query Match 30.8%; Score 44; DB 15; Length 27 Best Local Similarity 53.3%; Pred. No. 1.3e+02; Matches 8; Conservative 2; Mismatches 5; Indels
  APPLICANT: Yamamoto, Robert T.
APPLICANT: Xi, H. Roward
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
  Sequence 11541, Application US/10156761
Publication No. US2003011901841
GENERAL INFORMATION
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKANA, JUN
APPLICANT: HORIKANA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SKEAKI, YOSHIVOKI
APPLICANT: SKEAKI, YOSHIVOKI
APPLICANT: SKEAKI, YOSHIVOKI
APPLICANT: SAYAKI, YOSHIVOKI
APPLICANT: APTORI, MASAHIRA
ITILE GEFERNENCE: 249-262
FILE REFERNENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11541

MUMBER OF SEQ ID NOS: 15109
   : | || || |:
.LHVPDTFEGHFDGV 237
  Sequence 5704, Application US/09815242;
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Julith W.
APPLICANT: Zyskind, Julith W.
APPLICANT: Wall, Daniel
APPLICANT: Gari, Grant J.
   SDEFEGSFKGL 27
  ; ORGANISM: Streptomyces avermitilis US-10-156-761-11541
   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
   4 WAAQRYGRELRRMSD 18
   RESULT 15
US-09-815-242-5704
   US-10-156-761-115
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Gaps 0;

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September 15, 2003, 17:18:16 ; Search time 12.15 Seconds
(without alignments)
213.708 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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143
1 KNLWAAQRYGRELRRMSDEFEGSFKGL
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Perfect score:
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   Sequence:
   Run on:
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries pirl:\* pir2:\* pir3:\* PIR\_76:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|   |        | Description  | bad protein - mous | inter-alpha-trypsi | hypothetical prote |     | 2-dehydro-3-deoxy- | floral homeotic pr | spermidine/putresc | probable threonine | conserved hypothet | Ig kappa chain - h | annexin P35 - maiz | transforming prote | oxidoreductase, so | threonine synthase | Antho-RFamide neur |            | oxoglutarate dehyd |                   | 1      | ide    | hypothetical prote | orin | probable polyamine | inter-alpha-trypsi | hypothetical prote | DNA-directed RNA p | othe   | neuropeptide Pol-R | conserved hypothet |
|---|--------|--------------|--------------------|--------------------|--------------------|-----|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|-------------------|--------|--------|--------------------|------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|
|   | f      | TD           | 57                 | JC5575             | 9                  | 35  | S38185             | A42095             | C84338             | A96753             | E83517             | S40376             | T02975             | C36365             | F72289             | T08545             | A39172             | G82308     | F82668             | B96695            | T02961 | A44308 | T09486             | CD.  | T35440             | IYHU2              | T24806             | A81393             | G69510 | <b>S4</b> 3852     | AF2859             |
|   | 6      | 87           | 7                  | C)                 | 7                  | N   | ~                  | C3                 | ~                  | ~                  | 7                  | 7                  | 7                  | ~                  | N                  | N                  | 7                  | 7          | ~                  | 7                 | N      | N      | ~                  | ~    |                    |                    |                    |                    |        |                    |                    |
|   | 1      | Match Length | 204                | 946                | 223                | 946 | 370                | 232                | 374                | 516                | 453                | 134                | 314                | 206                | 220                | 526                | 334                | 597        | 2967               | 5138              | 314    | 435    | 1140               | 165  | 399                | 946                | 1164               | 1378               | 261    | 287                | 327                |
| æ | Query  | Match        | S                  | 7                  | $\sim$             | 7   | o                  | S                  | n                  | LO.                | ***                | m                  | m                  | $^{\circ}$         | m                  | m                  | 3                  | $^{\circ}$ | $^{\circ}$         | $^{\prime\prime}$ | (1     | 32.5   | (1                 | (1   | (1                 | (1                 | 32.2               | (1                 |        | 31.8               | $\Box$             |
|   |        | Score        | 138                | 54                 | 53                 | 53  | 52                 | 51                 | 20                 | 50                 | 49                 | 48.5               | ω.                 | 48                 | 48                 | 4                  | 47.5               | 47         | 47                 | 47                | œ.     | 46.5   | Ġ.                 | 46   | 46                 | 46                 | 46                 | 46                 | 5.     | 45.5               | 'n.                |
|   | Result | NO.          | Π.                 | 7                  | m                  | 47  | Ŋ                  | 9                  | 7                  | σο                 | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16         | 17                 | 18                | 19     | 20     | 21                 | 22   | 23                 | 24                 | 25                 | 26                 | 27     | 28                 | 29                 |
|   | Re     | 1            | Š                  | 9                  |                    |     |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |            |                    |                   |        |        |                    |      |                    |                    |                    |                    |        |                    |                    |

37.8%; Score 54; DB 2; Length 946; 34.6%; Pred. No. 9.9;

Query Match Best Local Similarity

| probable secreted | Mypurmerical proce | shotometra of | procesystem il oxy | manganese-stabilzi | conserved hypothet | conserved hypothet | sodium ion pumb ox | oxaloacetate decar | oxaloacetate decar | oxaloacetate decar | probable membrane | env polyprotein - | chromosome 5 GAP-1 | hypothetical prote | hypothetical prote |
|-------------------|--------------------|---------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|
| D97636            | C/ F#/ 3           | G00014        | 506/36             | AG2287             | F83201             | H95406             | B44465             | AB0509             | AE0909             | A28088             | S52675            | VCLJG4            | B59433             | T23005             | T22672             |
| (4)               | 4 C                | 9 (           | 7                  | ~                  | ~                  | ~                  | 7                  | 7                  | 7                  | N                  | 7                 | Н                 | ~                  | ~                  | 7                  |
| 327               | 000                | 200           | 7/3                | 273                | 295                | 346                | 591                | 591                | 591                | 596                | 715               | 864               | 915                | 1199               | 1217               |
| 8.7               | 0.1.0              | 0 1.0         | 31.5               | 31.5               | 31.5               | 31.5               | 31.5               | 31.5               | 31.5               | 31.5               | 31.5              | 31.5              | 31.5               | 31.5               | 31.5               |
| m r               |                    |               |                    |                    |                    |                    |                    |                    |                    |                    |                   |                   |                    |                    |                    |
| ហេដ               | . r.               | ``            | ۵.<br>د            | 45                 | 45                 | 45                 | 45                 | 45                 | 45                 | 45                 | 45                | 45                | 45                 | 45                 | 45                 |

## ALIGNMENTS

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Asserting the mouse bad protein - mouse bad protein - mouse bad protein - mouse bad protein - mouse c) Species was musculus (house mouse)

Cypecies: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999

CyAccession: A55671

Ryrang, B. 2. 21a, J. Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, J.995

Ayritle: Bad, a heterodimeric partner for Bol-x-L and Bol-2, displaces Bax and promot Axreference number: A55671; MUID:95136361; PMID:7834748

Axcession: A55671

Axcession: A55671

Axreference number: A55671; MUID:95136361; PMID:A84748

Axreferences preliminary; not compared with conceptual translation

Axreferences: 1-204 cANA.

Axreferences: GBL137296; NID:9639778; PIDN:AAA64465.1; PID:9639779

CXReywords: heterodimer
  inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster C; Species: Mesocricetus auratus (golden hamster)
C; Species: 32-sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JC5575; PC4485
R; Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Blochem: 122, 71-82, 1997
A; Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs
  All inhibitor heavy chain family.

A. Reference number: JC5574; MUD:97420688; PMID:9276673

A. Reference number: JC5574; MUD:97420688; PMID:9276673

A. Accession: JC5575

A. Molecule type: mRNA

A. Cross-references: DBBJ:D89286; NID:g1694689; PIDN:BAA13939.1; PID:g1694690

A. Residues: 1-946 < NAK>
A. Cross-references: DBBJ:D89286; NID:g1694689; PIDN:BAA13939.1; PID:g1694690

A. Residues: 1-946 < NAK>
A. Accession: PC4485

A. Molecule type: protein

A. Residues: 55-64; 140-146; 151-156; 424-447; 500-528; 577-605 < NA2>
C. Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important rolle for panceatic cancer.

C. Superfamily: inter-alpha-trypsin inhibitor complex component II

F: 261-264, 717-916/Disulfide bonds: #status predicted
   ô
  Gaps
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   0; Indels
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   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
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A; Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A; Reference number: S38185; MUID: 94078675; PMID: 8256522
A; Accession: S38185
A; Status: translation not shown
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A; Residues: 1-370 < DOID:
A; Residues: 1-370 < DOID:
A; Cross-references: GB:L20296; NID: 9311101; FIDN: AAA65607.1; PID: 9311102
B; Aljinovic, G:: Pohl, F. M:: Pohl, T. M.
Submitted to the Protein Sequence Database, August 1994
  A; Molecule type: DNA
Mysesiduse; 1.370 AAIG>
A; Residuse; 1.370 AAIG>
A; Cross-references: EMBL: 236118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR2
R; Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
B; Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
A; Title: A; F7-74, 1992
A; Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
A; Reference number: JN0322; MUID: 92225349; PMID: 1348717
  A,Molecule type: DNA
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A;Residues: 1-370 < ALJ>
A;Cross-references: ExBL:236118; NID:q536664; PIDN:CAA85212.1; PID:q536665; MIPS:YBR2
B;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
   A.Description: aldehyde-lyase; carbon-carbon lyase
A.Pathway aromatic amino acid biosynthesis; shikimate pathway
A.Note: first step in shikimate pathway
C.Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C.Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy
   ïs
  A,Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifun A;Reference number: A48651; WUID:93374850; PMID:8366040
  Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
  floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
N;Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42095; 552633; T47593
R;Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A;Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and A;Reference number: A42095; MUID:92154682; PMID:1346756
  ó
  Gaps
  R; Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
J. Bacteriol. 175, 5548-5558, 1993
  ö
   2; Length 370
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  A; Reference number: $45906
A; Accession: $46126
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   RESULT 3
D07760
hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
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C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C;Accession: D70760
R;Accession: D70760
R;Cole, S.T.; Beroch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Apares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.
A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: D70760
A;Accession: D70760
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  inter-alpha-inhibitor H2 chain - mouse
C; Species: Mus musculus (house mouse)
C; Accession: Sa4354
B; Chan, P; Risler, JL.; Raquence_revision 01-Sep-1995 #text_change 20-Aug-1999
B; Chan, P; Risler, JL.; Raquence, G.; Salier, J.P.
Biochen, J. 306, 505-512, 1995
A; Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: A; Reference number: S54353; MUID:95194326; PMID:7534067
A; Accession: S54354
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   333185
2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces of dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces of NyAlternate names: 3-deoxy-barabino-heptulosonate-7-phosphate synthase; DAHP synthase; Species: Saccharomyces cerevisiae 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002 C.Accession: S38185; S46126; S46130; JN0322; B48651
R.Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.
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   0;
  Score 53; DB 2; Length 946; Pred. No. 14;
   Length 223,
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58.8%;
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34.6%;
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Conservative
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Best Local Similarity 58.88

Matches 10; Conservative
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         Matches
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A;Status: preliminary A;Molecule type: mRNA

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Cippecies: Pseudomonas aeruginosa
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Cipte: 15-Sep-2000
Cipte: 15-Sep-2000
Cipte: 15-Sep-2000
Cipte: 15-Sep-2000
Cipte: 182517
Cipte: Complete genome Sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A; Reference number: A82950; MUID: 20437337; PMID: 10984043
A; Reference number: A82950; MUID: 20437337; PMID: 10984043
A; Status: preliminary
A; Status: Dreliminary
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A; Residues: 1-453
Cipte: Complete genome Seguence of Pseudomonas aeruginosa
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A; Recente complete genome sequence of Pseudomonas aeruginosa
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 200

Alvathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A., Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Alathors; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: A96733

A; Status: preliminary
  conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PAO
  ij
   ä
  A; Cross-references: GB: AE005173; NID: 95903070; PIDN: AAD55628.1; GSPDB: GN00141
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C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: 06-May-1995 #text_change 21-Jan-2000

C;Accession: 540376

R;Klein, R; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: 540312; MuID:94080891; PMID:8258341

A;Accession: 540376

A;Status: preliminary; translation not shown
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Pred. No.
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A;Gene: F3N23.1
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S40376
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C;Species: Halobacterium sp. NRC-1
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C;Accession: C8438
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
B;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MuID:20504483; PMID:11016950
A;Reference number: A84160; MUID:20504483; PMID:11016950
                         A;Cross-references: GB:M86357; NID:g166607; PIDN:AAA32740.1; PID:g166608
A;Experimental source: petals, stamens
A;Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBIP:82521)
R;Okamoto, H.; Tano, A.; Shiraishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A;Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid A;Reference number: S52633; MUID:95036018; PMID:7948893
   A;Note: T12E18.30
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
  R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A;Reference number: 224469
A;Reference number: 224469
  ó.
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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A; Exercence number: A72200; MUID:99287316; PMID:10360571
A;Reference number: A72200
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72289
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
   R;Curien, G.; Dumas, R.; Ravanel, S.; Douce, R. Press Lett. 390, 88-90, 1996
A;Title: Characterization of an Arabidopsis thaliana CDNA encoding an S-adenosylmethi A;Reference number: S71362; MUID:96314555; PMID:8706836
  threonine synthase (EC 4.2.3.1) precursor - Arabidopsis thaliana
N.Alternate names: protein F27813.80
S.Asternate names: protein F27813.80
C.Species: Arabidopsis thaliana (mouse-aar cress)
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002
C.Accession: T08545, S71362, S74307
S.Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, May 1999
A.Reference number: Z16442
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  A, Accession: 571362
A, Molecule type: mRNA
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   Query Match
  RESULT 13
F72289
  RESULT 14
   g
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  δŽ
   δ
   C; Accession: C36355
R; Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A; Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhib A; Reference number: A36365; MUID:91061774; PMID:1701021
A; Reference number: A36365
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F; 123-126/Region: GTP-binding SAK/L motif
F; 153-126/Region: GTP-binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
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C;Accession: T02975
R;Battey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A;Title: CDNA isolation and gene expression of maize annexins P33 and P35.
A;Reference number: 214796, MUID:97092863; PMID:8938425
A;Accession: T02975
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   transforming protein homolog MRAS3 - Rhizomucor racemosus
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C) Keywords: heterotetramer; immunoglobulin
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   δž
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A39172
Antho-Remaids neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica)
C. Accession: A39172
Antho-Remaids neuropeptide 19 repeat precursor - sea anemone (Calliactis parasitica)
C. Accession: A39172
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C. Accession: A39172
A. Accessi
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 15, 2003, 17:16:55; search time 6.36429 Seconds (without alignments) 199.507 Million cell updates/sec Run on:

US-09-544-664-56 143 1 KNIWAAQRYGRELRRMSDEFEGSFKGL 27 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           |        | Description  | -         |     | Q92934 homo sapien | _    | Q61703 mus musculu | O62992 ledum palus |      |                   |      | P35632 arabidopsis |      |      | P22280 rhizomucor |      |      |      |      |      |      |      |      |      |      | P21259 polyorchis |       | Q9p869 kluyveromyc |      | klebs | homo s | simis ( | , £5  |       | Q95gj0 gaultheria |
|-----------|--------|--------------|-----------|-----|--------------------|------|--------------------|--------------------|------|-------------------|------|--------------------|------|------|-------------------|------|------|------|------|------|------|------|------|------|------|-------------------|-------|--------------------|------|-------|--------|---------|-------|-------|-------------------|
| SUMMARIES |        | a            | BAD_MOUSE |     | BAD_HUMAN          |      |                    | MATK               | MATK | MATK              |      | AP3_ARATH          |      |      | RAS3_             |      |      | ٠.   |      |      |      |      |      |      |      |                   | PSB0_ |                    | DCOA |       |        |         | CE05_ | LML1_ | . MATK_GAUPR      |
|           |        | ength DB     |           |     |                    |      |                    |                    |      |                   |      |                    |      |      |                   |      |      |      |      |      |      |      |      |      |      |                   |       |                    |      |       |        |         | 915 1 |       |                   |
| о¥        | Query  | Match Length | 96.5      | •   | σ,                 | 37.8 |                    |                    | ė.   | 36.7              | 36.4 | 35.7               | 35.7 | 34.3 | 33.6              | 33.6 | 33.6 | 33.6 | 33.2 | 33.2 | 32.9 | 32.5 | 32.5 | 32.2 | 32.2 | 31.8              | 31.5  | ш                  | 31.5 | 31.5  | ٦      | Н       | 31.5  | 31.5  | 31.1              |
|           |        | Score        | 138       | 138 | 114                | 54   |                    | $^{\circ}$         | 52.5 | $^{\prime\prime}$ | 52   | 51                 | 51   | 49   | 48                | 48   | 48   | 48   | ~    | 47.5 |      | Q    | 46.5 | 46   |      | 45.5              | 45    | 45                 | 45   | 45    | 45     | 45      | 45    |       | 44.5              |
|           | Result | No.          | 2/ 1      | Z   | m                  | 4    | N                  | 9                  | 7    | 80                | σ    | 10                 | 11   | 12   | 13                | 14   | 15   | 16   | 17   | 18   | 19   | 20   | 21   | 22   | 23   | 24                | 25    | 56                 | 27   | 28    | 29     | 30      | 31    | 32    | 33                |

| Q9gig3 lillium tsin | P33900 salmonella<br>O54918 mus musculu | 088498 rattus norv | Q8x9c6 escherichia | P50465 escherichia | Q8z8d2 salmonella | Q8zqu6 salmonella | 033925 thermotoga | P27757 simian immu | P27977 simian immu |
|---------------------|-----------------------------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|
| MATK_LILIS          | NUOG_SALTY<br>BIM_MOUSE                 | BIM_RAT            | END8_ECO57         | END8_ECOLI         | END8_SALTI        | END8_SALTY        | SYM_THEMA         | ENV_SIVA1          | ENV_SIVAG          |
|                     | 4 ~ ~                                   | ~1                 | -                  | 1                  | <del>, -</del> 1  | H                 | Н                 | Н                  | Н                  |
| 512                 | 907                                     | 196                | 262                | 262                | 262               | 262               | 629               | 768                | 877                |
| 31.1                | 31.1                                    | 30.8               | 30.8               | 30.8               | 30.8              | 30.8              | 30.8              | 30.8               | 30.8               |
| 44.5                | 44.5                                    | 44                 | 44                 | 44                 | 44                | 44                | 44                | 44                 | 44                 |
| 34                  | 386                                     | 38                 | 36                 | 40                 | 41                | 42                | 43                | 44                 | 45                 |

## ALIGNMENTS

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   0;
  D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in the rat brain.";
  S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION, INTERACTS WITH
  Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl.×LlSel-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
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PKB).
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   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
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          major site of protein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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0; Mismatches 0; Indels
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  MEDLINE=98194755; PubMed=9535132;
  Neurosci. Lett. 243:137-140(1998).
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MOD_RES
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MUTAGEN
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   S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS. NO EFFECT ON HETERODIMERIZATION
WITH BCLZ NOR WITH PROTEIN P11.
SDAGGR -> ERRORK (IN REF. 1).
7AFA7IDAE9CF4A8I CRC64;
   Bcl-
  -> EELTYSVEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
EVAMFPLRYWTALRRLC (in isoform Beta).
   -:- FUNCTION: Promotes call death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with Bax. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-!- SUBONIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w Also binds protein SIOA10. The Ser-137 phosphorylation for mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).
  Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-137 is the major site of AKT/PKB phosphorylation, Ser-156 the major site of protein kinase A (CAPK) phosphorylation (By
  TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more
  LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
  DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bol-2 family.

PTM: Phosphorylated on Ser-113 in response to survival stimuli.
Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D., "Functional characterization of two splice variants of rat BAD and their interaction with BGL-win sympathetic neurons."; Mol. Cell. Neurosci. 17:97-106(2001).
   (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
  BH3.
PHOSPHORYLATION (BY PKA AND PKB)
   similarity).
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 PAMILY.
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22228 MW;
  ALTERNATIVE PRODUCTS
  137
  156
   205
   113
  137
   29
205 AA;
   abundant form.
  137
  156
   166
   113
  137
  Name=Alpha
   Name=Beta;
   Apoptosis;
   CONFLICT
  VARSPLIC
   MOD_RES
  MUTAGEN
  MUTAGEN
   MOD_RES
  MOD_RES
  DOMAIN
  <u>.</u>..
```

SEQUENCE

```
Query Match
0
   Ransberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rilsberg R.L., Zeeberg B., Buetow K.H., Scheefer C.F., Blat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellanon N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rahas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J.S., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Human and mouse cDNA sequences.",
   SEQUENCE FROM N.A.
Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
"A human protein that interacts with Bcl-2 and have homology to mouse
   092934; Ol4803; Ol4803; Ol-NOV-1997 (Rel. 35, Created)
11-OCT-2001 (Rel. 40, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component 6) (BCl-XL/BCl-2 associated death promoter) (BCL2-like 8 protein).
BAD OR BBC6 OR BCL2L8.
   Gaps
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  MEDLINE-98049554; Pubmed-9388232; Ottilie S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G., Chang S., Weeks S., Fritz L., Oltersdorf T.; "Dimerization properties of human BAD."; J. Biol. Chem. 272:30866-30872(1997).
   0
                  Length 205;
  MEDLINE-97083574; PubMed-8929532;
Wang H.-G., Rapp U.R., Reed J.C.;
"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
  0; Indels
   Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
  Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
   Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                  DB 1; L
1.8e-13;
  SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
  168 AA.
  0; Mismatches
                  Score 138;
Pred. No.
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   SEQUENCE FROM N.A., AND DIMERIZATION.
  TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
  human and mouse cDNA sequences.
                96.5%; £
      Query Match
Best Local Similarity 100.0
  STANDARD;
  Cell 87:629-638(1996).
  Homo sapiens (Human)
  TISSUE-Bone marrow;
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
  BAD HUMAN
   Proc.
   BAD.
   RESULT 3
  HIDDD THE SERVICE OF 
   QΥ
  q
```

```
Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
R Feeik S.W.;
TRationale for Bcl-xL/Bad peptide complex formation from structure,
mutagenesis, and biophysical studies.",
Frotein Sci. 9:2528-2534(2000).
The Promotes of the Structure of the Promotes of the Structure of heterodimerization of these proteins with BAX. Can reverse the of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

C. SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100AlO (By similarity).

CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
  phosphorylation, loades to the ortoplasm.

-: TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-: DAMAN: Intact BH3 domain is required by BIK, BID, BAK, BAD. BAX.
BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
-: PIM: Phosphorylation on Ser-75 in response to survival stimuli.
Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118 a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival.
Ser-99 is the major site of ARV/PKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by similarity: Contains 1 Bcl-2 homology 3 (BH3) domain.
-: SIMILARITY: Contains 1 Bcl-2 FAMILY.
-: CAMILARITY: BELONGS TO THE BCL-2 FAMILY.
-: CAMILARITY: BELONGS TO THE BCL-2 FAMILY.
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STRUCTURE BY NMR OF 103-127.

BEDLINE-21073561; PubMed-11206074;
PETTOS A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
   PHOSPHORYLATION (BY PKA AND PKB) (BY
  (BY
  PHOSPHORYLATION (BY PKA AND PKB) (BY
  PHOSPHORYLATION (BY PKA AND PKB)
  SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
   Score 114; DB 1; Length 168;
   Polymorphism; 3D-structure.
  69FD8D27DDEE3241 CRC64;
   (in dbSNP:3729933)
  NAS.
   GO: GO: 0005737; C: cytoplasm; NAS.
GO: GO: 0005741; C:mitochondrial outer membrane; 1GO: GO: 0005518; P:protein binding activity; NAS.
GO: GO: GO: REPORT P: protein binding activity; NAS.
GO: GO: GO: P: proprotic program; TAS.
GO: GO: 0006917; P:induction of apoptosis; NAS.
  A -> S (in dbSNP:
/FTId=VAR_015380.
  SIMILARITY).
  SIMILARITY).
  SIMILARITY
  EMBL; U66879; AAB36516.1; ALT_FRAME.
   InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
   EMBL; AF021792; AAB72092.1; -.
EMBL; AF031523; AAB88124.1; -.
EMBL; BC001901; AAH01901.1; -.
  18392 MW;
   79.78;
   Phosphorylation;
   in position 64 and 91.
  124
75
  66
  118
  107
   121
  Genew; HGNC:936; BAD. MIM; 603167; -.
  PDB; 1G5J; 07-FEB-01
   106
168 AA;
  118
  107
  66
   Apoptosis;
  SEQUENCE
   MOD_RES
  MOD_RES
  MOD_RES
  VARIANT
   HELIX
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us-09-544-664-56.rsp

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SMART; SM00327; VWA; 1.
  Matches
   RESULT
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   δŽ
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                   ö
  Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
Molecular cloning and sequencing of cDNAs encoding three heavy-chain
precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
implications for the evolution of the inter-alpha-trypsin inhibitor
   SUBUNIT: I'ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HI, #2 OR H3) AND ONE LIGHT CHAIN,
BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF HI, H2
AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
BIKUNIN, AND PRE-ALPHA-LIKE INHIBITOR (P-ALPHA-LI) OF H2 AND
PHW: HEAVY CHAINS ARE INTERLINEED WITH BIKUNIN VIA A CHONDROITIN
F-SULPATE BRIDGE TO THE THERR C-TERMINAL ASSARVATE (SY
                   Gaps
   FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURPACES IN TISSUES TO REGULATE THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
   15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (HC2).
   Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.",
J. Biochem. 120:145-152(1996).
   Eukaryota; Metazoa; Chordata; Creniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
   SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605.
                   0;
                   Indels
                 'n
Pred. No. 5.8e-10;
  946 AA.
  SIMILARITY: BELONGS TO THE ITH FAMILY. SIMILARITY: Contains 1 VWFA domain.
                   Mismatches
  (Golden hamster).
   103 NLWAAQRYGRELRRMSDEFVDSFK 126
   2 NLWAAQRYGRELRRMSDEFEGSFK 25
   PRT;
  TISSUE-Liver;
MEDLINE-97420688; PubMed-9276673;
   MEDLINE=97018241; PubMed=8864857;
                 .
0
   (Rel. 36, Created)
   Biochem. 122:71-82(1997).
   EMBL; D89286; BAA13939.1; -.
91.78;
   InterPro, IPR006587; VIT.
InterPro, IPR002035; VWF_A.
Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
                   22; Conservative
  STANDARD;
   PIR; JC5575; JC5575.
  Mesocricetus auratus
   heavy chain family.
   Best Local Similarity
  SEQUENCE FROM N.A.
  NCBI_TaxID=10036;
  SIMILARITY).
  SIMILARITY)
   TISSUE-Plasma;
  Mesocricetus.
   15-JUL-1998
   ITH2_MESAU
   ITH2 MESAU
                   Matches
   AND
   δ
   g
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   ö
   BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
   SUBDIT: 1.Alepha-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (HI, HZ OR H3) AND ONE LIGHT CHAIN, BIRUMIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF HI, HZ AND BIRUMIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF HZ AND BIRUMIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIRUMIN. INTER-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIRUMIN. ILSGUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
   Gaps
  PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
   CHONDROITIN 4-SULFATE, CROSS-LINK SITE (BY SIMILARITY).
V -> Y (IN REF. 2).
V -> I (IN REF. 2).
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  15-JUL-1998 (Rel. 36, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H2 precursor (III heavy chain H2) (Inter-alpha-tinhibitor heavy chain 2).
  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
  (POTENTIAL)
   ó
   (POTENTIAL
           Serine protease inhibitor; Repeat; Signal; Multigene family;
   Score 54; DB 1; Length 946;
   Indels
  106580 MW; CA8BF565458E7B2E CRC64;
   12;
   N-LINKED (GLCNAC. .. N-LINKED (GLCNAC. ..
  946 AA.
  Pred. No. 3.7;
   -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
   SIMILARITY.
   5; Mismatches
  -!- SIMILARITY: Contains 1 VWFA domain.
  212 NVWIVELQGMRFLHVPDTFEGHFQGV 237
   POTENTIAL
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  PRT;
   H2.
BY SJ
VWFA.
   Created)
   37.8%;
   -! - PTM: HEAVY CHAINS ARE
VWFA; 1.
   9; Conservative
  STANDARD;
  510
595
   946
4468
1118
263
445
702
  (Rel. 36, (Rel. 36, (Rel. 41,
  946 AA;
  Best Local Similarity
  SEQUENCE FROM N.A.
 PROSITE; PS50234;
   NCBI_TaxID=10090;
   703
308
1118
263
445
702
  SIMILARITY)
                            Glycoprotein
  5-JUL-1998
  TTH2_MOUSE
  CARBOHYD
CARBOHYD
  CARBOHYD
  SEQUENCE
  Query Match
   CONFLICT
  CARBOHYD
  CONFLICT
  BINDING
   PROPEP
CHAIN
   PROPEP
  DOMAIN
   SIGNAL
  RESULT 5
ITH2 MOUSE
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   Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoldeae; Rhodoreae; Rhododendron. NCBI_TaxID=49622;
   -I-FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-I-SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
  7;
  7
   SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
   Score 52.5; DB 1; Length 506; Pred. No. 3.1;
  Length 506;
  Indels
   EMBL; AB012741; BAA25862.1; -.
InterPro; IPR000442; Intron.maturse2.
InterPro; IPR00366; MatK.N.
Pfam; PF01348; Intron.maturas2; 1.
Pfam; PF01844; MatK.N; 1.
Pfam; PF01844; MatK.N; 1.
SEQUENCE 506 AA, 60534 WW; ADA44B25E92436E8 CRC64;
  "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
   CFEA926307DAC85E CRC64;
  .,
8
  8;
   DB 1;
   | :||| :||| | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
   | :||| : || | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   AA.
   36.7%; Score 52.5; DE 37.5%; Pred. No. 3.1; ive 5; Mismatches
  5; Mismatches
EMBL; AB012751; BAA25872.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60412 MW; CFEA9263
  Rhododendron ferrugineum (Alpenrose).
   PRT;
  Maturase K (Intron maturase).
  36.7%;
37.5%;
  Ouery Match
Best Local Similarity 37.59
Matches 12; Conservative
  12; Conservative
  STANDARD;
  Best Local Similarity
  SUBFAMILY.
  Chloroplast.
  MATK_RHOTS
062991;
  MATK_RHOFR
  Yukawa T.;
  Query Match
  MATK_RHOTS
ID MATK_RI
AC 062991
  MATK_RHOFR
  Matches
  RESULT 8
  RESULT 7
        g
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   ö
   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to licenses[sib.sib.ch).
   BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
   Gaps
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   N-LINKED (GLCNAC. . .) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
  "Investigation of sectional relationships in the genus Rhododendron (Ericaceae) based on matK sequences."; Shokubutsu Kenkyu Zasshi 73:143-154(1998).
-:- FUNCTION: Probably sists in splicing chicroplast group II introns (By similarity).
-:- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
   ö
  Serine protease inhibitor; Repeat; Signal; Multigene family;
  DB 1; Length 946;
  SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
   5; Mismatches 12; Indels
   (BY SIMILARITY).; 40DB6716433ED9DC CRC64;
   (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
  5.2;
   506 AA
  SIMILARITY.
  37.1%; Score 53;
  212 NVWIIEPQGMRFLHVPDTFEGHFQGV 237
   POTENTIAL
   2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
   Pred. No.
   PRT;
  VWFA.
  Ledum palustre (Wild rosemary).
  MM:
  Maturase K (Intron maturase).
   EMBL; X70392; CAA49842.1; -.
   34.68;
  PIR, S54354, S54354.
MCD, MGI:96619, Itih2.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
  105927
   Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
  Best_Local Similarity 34.6
Matches 9; Conservative
   STANDARD;
  946 AA;
  NCBI_TaxID=75583;
   19
  SUBFAMILY.
   15-SEP-2003 (
15-SEP-2003 (
15-SEP-2003 (
   Glycoprotein.
SIGNAL
   Chloroplast.
   MATK_LEDPA
  DOMAIN
CARBOHYD
  SEQUENCE
  Query Match
   CARBOHYD
  BINDING
  PROPEP
CHAIN
  PROPEP
  RESULT 6
MATK_LEDPA
       δλ
  S
S
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Gaps

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Kuenzler
  Matches
  RESULT 10
  AP3_ARATH
      Q
  δŏ
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  ij
   MEDINE-92225349; PubMed=1348717; Kuenzler M., Paravicini G., Bgli C., Irniger S., Braus G.H.; Kuenzler M., Paravicini G., Bgli C., Irniger S., Braus G.H.; "Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";
  Gaps
   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-barabino-heptulosonate 7-phosphate synthase).
ARO4 OR YBR249C OR YBR1701.
   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  7;
  SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
   36.7%; Score 52.5; DB 1; Length 506; 37.5%; Pred. No. 3.1; Live 5; Mismatches 8; Indels 7
  Chloroplast.
A; 60569 MW; AEE12FF8809C223E CRC64;
   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   370 AA.
   Saccharomyces cerevisiae (Baker's yeast).
   InterPro; IPR000442; Intron_maturse2. InterPro; IPR002866; Matk_N. Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
   PRT;
   01-OCT-1993 (Rel. 27, Created)
   EMBL; AB012750; BAA25871.1; -.
                                       Maturase K (Intron maturase).
  Rhododendron tsusiophyllum.
   Query Match
Best Local Similarity 37.55
Matches 12; Conservative
   STANDARD;
   Gene 113:67-74(1992).
   REVISIONS TO 205-207.
  506 AA;
   SEQUENCE FROM N.A.
  NCBI_TaxID=49629;
  mRNA processing;
   NCBI_TaxID=4932;
  SUBFAMILY
             28-FEB-2003
28-FEB-2003
  Chloroplast
  AROG_YEAST
  SEQUENCE
  Yukawa T
   AROG_YEAST
   QΣ
   셤
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  EMBL; X61107; CAA43419.1; -.
EMBL; L20296; AAA65607.1; -.
EMBL; S34815; CAA65212.1; -.
PIR; S34815; S38185.
SGD; S0000455; ARC4.
GO; CO:0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase . . .; IDA.
  Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSFECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ERYTHROSFE4-PROSPHATE (EAP) GIVING RISE TO 3-DEOXY-D-
ARABINO-HEPPULOSONARE-7-PHOSPHATE (DAHF).
-!- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
   MEDLINE-94078675; PubMed-8256522;
Doignon F., Biteau N., Aigle M., Crouzet M.;
"The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative Ammase in a vaset ".
   Gaps
   PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
  AP3_ARATH STANDARD; PRT; 232 AA.
P35632; Q39003; Q8LB79; Q9S7Q3; Q9SQ14; Q9SQ15; Q9SQ16; Q9SQ17;
Q9SQ18; Q9SQ19; Q9SQ20; Q9SQ21; Q9SQ22; Q9SX13;
  0
   phosphate + phosphate = phosphoenolpyruvate + D-erythrose phosphate + H(2)0.
ENZIME REGULATION: INHIBITED BY TYROSINE.
  -!- INDUCTION: By amino acid starvation.
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
  Lyase; Multigene family.
  Length 370;
  Indels
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
   Pfan. PP00733; DAHP_synth_1; 1.
ProDom; PD005060; ArcFGH; 1.
Arcmaric amino acid biosynthesis; Lyase; Multigene fami SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
  :9
   36.4%; Score 52; DB 1; 47.6%; Pred. No. 2.7;
  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
Floral homeofic protein APETALA3.
AP3 OR AT3G54340 OR TIZE18_30.
  5; Mismatches
  80 DLEAAQEYALRIKKLSDELKG 100
  2 NLWAAQRYGRELRRMSDEFEG 22
  InterPro; IPR006219; AroFGH.
InterPro; IPR006218; DAHP1/KDSA.
  Local Similarity 47.6
tes 10; Conservative
   dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   first step.
  STRAIN-S288c;
  STRAIN=S288c;
  Query Match
```

```
RA Balanoubat M., Lemcker M., Raceger M., Onserge W., Unseld M.,
RA Salanoubat M., Lemcker M., Reger M., Derez-Alonso M., Obermaier B.,
Ratrmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L., Macher C., Erottier F.,
RA Besimone V., Choisne N., Ariquenave F., Robert C., Erottier F.,
RA Mincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Murmbach E., Drzonek H., Erich H., Jordan N., Bangert S.,
R. Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Winschen E., Drzonek H., Erich H., Jordan N., Bangert S.,
R. Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Roorey T., Ladde M., Berger-Lalauro C., Purnelle B., Masuy D.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Monfort A., Malls A., Otterback T., Pullon L.J., Jenkins J.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Rooney T., Raals A., Waits A., Otterback T., Pullon L.J., Jenkins J.,
RA Greasy T.H., Haas B., Maits A., Otterback S.L., White O., Venter J. C.,
RA Freezer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Fraser C.M., Matsumoto M., Matsumo A., Muraki A.,
RA Sasamoto S., Katola M., Matsumoto M., Matsuno A., Muraki A.,
RA Sasamoto S., Makazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Jamada M., Yasuda M., Tabata S.,
RA Watanabe A., Jamada M., Yasuda S. Ottor Plant Arabidopsis
  STRAIN-CV. Bla-1, CV. Bretagny, CV. Bs-1, CV. Bu-0, CV. Bu-2, CV. Chill, CV. Columbia, CV. Corsacalla-1, CV. Cvi-0, CV. Columbia, CV. Corsacalla-1, CV. Cvi-0, CV. Gr-3, CV. Ji-1, CV. Kas-1, CV. Kent, CV. Landsberg erecta, CV. Li-3, CV. Li-8, and CV. Lisse, MEDILINE-99126449; PubMed-9927444; Purugganan M.D., Sudith J.I.; "Molecular population genetics of floral homeotic loci: departures from the equilibrium-neutral model at the APETALA3 and PISTILLATA genes of Arabidopsis thallana."; denetics 151:839-848(1999).
  MEDLINE-92154682; PubMed=1346756;
Jack T., Brockman L.L., Meyerowitz E.M.;
"The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
box and is expressed in petals and stamens.";
Cell 68:683-697(1992).
   Okamoto H., Yano A., Shiraishi H., Okada K., Shimura Y.; "Genetic complementation of a floral homeotic mutation, apetala3, with an Arabidopsis thaliana gene homologous to DEFICIENS of
  Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
  Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.; Furnann K.; Full-lengh Companited (MAR-2002) to the EMBL/GenBank/DDBJ databases.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
   STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
  STRAIN-cv. Landsberg erecta;
MEDLINE-95036018; PubMed-7948893;
  Plant Mol. Biol. 26:465-472(1994).
  SEQUENCE FROM N.A., AND VARIANTS.
  Nature 408:820-822(2000).
   SEQUENCE FROM N.A. STRAIN=cv. Columbia;
   [2]
SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   Antirrhinum majus.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
                 NCBI_TaxID=3702;
   rissue-Petal
   thaliana.
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   Nature 409:255-529(2001).

Nature 409:255-529(2001).

-!- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with PISTILIAMA that is required for autoreadiation of both AP3 and PI genes. AP3/PI heterodimer interacts with APETALAI or SEPALLATA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower
   PubNed-8643482;
Riechmann J.L., Krizek B.A., Meyerowitz E.M.;
"Dimerization specificity of Arabidopsis MADS domain homeotic proteins
APETALA1, APETALA3, PISTILLAYA, and AGAMONS.";
Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
   STRAIN-cv. Columbia; MEDLINB-99311297; PubMed-10382288; MEDLINE-99311297; PubMed-10382288; MEDLINB-99311297; Proger N., Pelletier G.; Pervelopment of amplified consensus genetic markers (ACGM) in Brassica napus from Arabidopsis thallana sequences of known biological
   Krizek B.A., Meyerowitz E.M.; "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function.";
  Honna T., Goto K.; "Complexes of MADS-box proteins are sufficient to convert leaves into
   SUBUNIT: Forms an heterodimer with PISTILLATA, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to
  -:- TISSUE SPECIFICITY: Expressed in petals and stamens.
-:- INDUCTION: Positively regulated by the meristem identity proteins
APETALAI and LEAPY with the cooperation of UFO.
-:- MISCELLANBOUS: Mutations in AP3 cause transformation of petals
  Ng M., Yanofsky M.F.;
"Activation of the Arabidopsis B class homeotic genes by APETALAl.";
Plant Cell 13:739-753(2001).
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RKEN Arabidopsis full length colve (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC)."; submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
   into sepals and stamina into carpels.
  -!- SIMILARITY: Contains 1 K-box dimerization domain.
  SUBCELLULAR LOCATION: Nuclear.
   EMBL, M86357; AAA32740.1; -.
EMBL, D21125; BAA04665.1; -.
EMBL, AF115798; AAD51887.1; -.
EMBL, AF115799; AAD51888.1; -.
  Development 122:11-22(1995).
   FROM N.A.
   Genome 42:387-402(1999).
   SEQUENCE OF 36-128 F. STRAIN-cv. Columbia;
   GENETIC REGULATION.
  form complexes
  CHARACTERIZATION.
   CHARACTERIZATION.
  PubMed=11283333;
  PubMed=11206550;
   floral organs.";
   development.
   PubMed=8565821;
   function.
  FUNCTION.
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statcheon M., Soarse M.B., Bonaldo M.F., Casavand T.E., Schect T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.R., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.R., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ratchering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ratchering M., Madan A., Schein J.E., Jones S.J.M., Marra M.A., Reneration and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903(2002).

Proc. MallarRity: Belongs to the FAMJ3 family.
  SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Nature 406:959-964(2000).
   Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
  35.7%; Score 51; DB 1; Length 851; 41.7%; Pred. No. 9.3;
  8; Indels
   189 256 GLU-RICH.
851 AA; 97054 MW; C2B26669FB6DB2CE CRC64;
  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA recombination protein rmuC homolog.
  6; Mismatches
  : || |: ::||:| || :| 3782 EQLWKARAEKKILRKMIREFEEAF 805
   RHO-GAP
  1 KNLWAAQRYGRELRRMSDEFEGSF 24
  EMBL; BC031465; AAH31465.1; -. InterPro; IPR000198; RhoGAP.
   Pseudomonadaceae; Pseudomonas
   PROSITE; PS50238; RHOGAP; 1.
   Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1
  Local Similarity 41.7
   STANDARD;
   GTPase activation.
   23
189
   NCBI_TaxID=287;
   RMUC OR PA1031.
  RMUC_PSEAE
Q914U3;
   SEQUENCE
   Query Match
   RMUC_PSEAE
  Matches
   RESULT 12
        | R SWART; SW00432; MADS; 1.
| R PROSITE; PS00350; MADS_BOX_1; 1.
| R PROSITE; PS000566; MADS_BOX_2; 1.
| R PROSITE; PS00066; MADS_BOX_2; 1.
| POWALN 93 165 K-BOX.
| FT DOMAIN 93 165 K-BOX.
| FT DOMAIN 75 164 K-POX.
| FT VARIANT 47 47 M -> T (in strain cv. Lisse).
| FT VARIANT 61 61 M -> D (in strain cv. Corsacalla-1).
| FT VARIANT 73 73 7 -> S (in strain cv. Lis).
| FT VARIANT 109 109 L -> V (in strain cv. Lis).
| FT VARIANT 115 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
| FT VARIANT 115 115 E-> K (in strain cv. Corlacalla-1).
  MADS.

K-BOX.

K-BOX.

COLLED COIL (POTENTIAL).

K -> R (in strain cv. Lisse).

M -> T (in strain cv. Corsacalla-1).

T -> S (in strain cv. Liss).

L -> V (in strain cv. Liss).

E -> K (in strain cv. Corsacalla-1).

Corsacalla-1).

L -> V (in strain cv. Kas-1).

E -> K (in strains cv. Chi-1 and cv. Gr-3).
   STRAIN=FVB/N;
MEDINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
   35.7%; Score 51; DB 1; Length 232; 44.4%; Pred. No. 2.3;
   [5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
   Pred. No. 2.3;
3; Mismatches
   7 ORYG-----RELREMSDEFEGSFK 25
  EMEL, AFILSGII; AADS1900.1; EMEL, AFILSGII; AADS1900.1; EMEL, AFILSGII3; AADS1900.1; EMEL, AFILSGII3; AADS1901.1; EMEL, ALGASTI, AADS1903.1; EMEL, ALGASTI, CABRI799.1; EMEL, AYOR0769; AAM64919.1; EMEL, AYOR0397; AAM64919.1; EMEL, AYOR0397; AAL48993.1; EMEL, AYOR0597; AAL9893.1; EMEL, AYOR0541; AAL095, AAUSTST.1; PIR, A42095, PII746; IMNM.

TRANSFAC; T01776; ...
   TRANSFAC; T01776; -.
InterPro; IPR002487; TF.Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
    EMBL, AFI15803, AAD51892.1;
EMBL, AFI15804, AAD51893.1;
EMBL, AFI15805, AAD51894.1;
EMBL, AFI15806, AAD51895.1;
EMBL, AFI15807, AAD51895.1;
EMBL, AFI15808; AAD51896.1;
EMBL, AFI15808; AAD51896.1;
   Best Local Similarity 44.4 Matches 12; Conservative
   STANDARD;
  Protein C5orf5 homolog.
  SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
                          AF115801;
AF115802;
   AF115810;
   CE05_MOUSE
Q8K2H3;
   Query Match
  CSORFS
   EMBL;
  CE05_MOUSE
  RESULT 11
      g
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Gaps

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Gaps

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   MEDLINE=9928/316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Exidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
  phospho-D-gluconate.
-!- PATHWAY: Pentose phosphate pathway: second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACOSAMINE-6-PHOSPHATE.
ISOMERASE FAMILY: 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
  PHOSPHOGLUCONATE.
-!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
  Thermotoga maritima,
Bacteria, Thermotogae, Thermotogales; Thermotogaceae, Thermotoga.
   33.6%; Score 48; DB 1; Length 205; 62.5%; Pred. No. 5.6; tive 2; Mismatches 4; Indels
  GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBALE).
FARNESYL (BY SIMILARITY).
W; DBF086466F090F50 CRC64;
  -:- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
   9B0FD07EE01E60C3 CRC64;
  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-PED-2003 (Rel. 41, Last annotation update)
6-Phosphoglucomolactomase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR TM1154.
   DB 1;
   Score 48;
Pred. No. 6
   GTP-binding; Prenylation; Lipoprotein. NP_BIND 16 23 GTP (BY S
  Interpro; IPR006148; Gluc_gal_isom.
Interpro; IPR005900; Phosphogluconlac.
   Pfam; PF01182; Glucosamine_iso; 1.
TIGRFAMS; TIGR01198; pgl; 1.
                        SMART; SM00173; RAS; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
   Hydrolase; Complete proteome.
SEQUENCE 220 AA; 25325 MW;
   23408 MW;
  PRINTS; PR00449; RASTRNSFRMNG.
  EMBL; AE001772; AAD36230.1; -.
  168 REIRRMNKEQEGRSKG 183
  33.6%;
   34.8%;
  11 RELRRMSDEFEGSFKG
  Conservative
   STANDARD;
   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
   23
67
125
46
202
  PIR; F72289; F72289.
  122 1
38
202 2
205 AA;
  Query Match
Best Local Similarity
   Similarity
  NCBI_TaxID=2336;
   Query Match
Best Local Simi
Matches 10;
   6PGL_THEMA
Q9X0N8;
   SEQUENCE
   NP_BIND
NP_BIND
DOMAIN
  LIPID
   6PGL_THEMA
   RESULT 14
  DR DR DR DR LATE FIT FIT SQ
  qq
   δŽ
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  MEDLINE=91061774; Pubmed=1701021;

Casale W.L., McConpell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;

Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibits striking similarity to human ras genes:";

Mol. cell. Biol. 10:6654-6663(1990).

-!- BRZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-ACTIVATED BY A GTPASE-ACTIVATED.
   Gaps
  SIMILARITY: BELONGS TO THE SMALL GIPASE SUPERFAMILY. RAS FAMILY.
  SUBCELLULAR LOCATION: Plasma membrane.
DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
  Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
Eukaryota, Fungi, Zygomycota, Zygomycetes, Mucorales, Mucoraceae;
   5
FUNCTION: Involved in DNA recombination (By similarity).
  DB 1; Length 453;
   2; Indels
   Pfam; PF02646; RmuC; 1.

DAMA recombination; Coiled coil; Complete protecme.

DOMAIN 16 201 COILED COIL (POTENTIAL).

SEQUENCE 453 AA; 51539 MW; 1E7EA97E82EC5E4B CRC64;
   01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
  205 AA.
   Pred. No. 9.3;
                     SIMILARITY: BELONGS TO THE RMUC FAMILY.
  Mismatches
  Score 49;
  PRT;
  HSSP; PO1112; 1PLL.
InterPro; IPR003577; GTPase_Ras.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005255; Small_GTP.
   4 WAAQRYGR -- ELRRMSDE 19
  EMBL; AE004535; AAG04420.1; -.
   WASERQGREEELRRLASE 82
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InterPro; IPR003798; DUF195.
  Best_Local Similarity 55.6
Matches 10; Conservative
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  GERMLING AND YEAST
  Ras-like protein 3.
   SEQUENCE FROM N.A.
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  RAS3_RHIRA
  65
   Query Match
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RAS3\_RHIRA

ó qq DD BRAND DRAND DRA

Length 220;

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Hasp; 0967B5; 1E5X.

R HSSP; 0967B5; 1E5X.

R InterPro; IPR001926; M-Gargume_beta.

DR InterPro; IPR004450; Thr_synthase.

DR Pfam: PF00291; PALP; 1.

DR TIGREMAM; TIGRO260; Thrc; 1.

DR PROSTE; PS00165; DEHYDRATASE.SER_THR; 1.

RW Threonine blosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme; KW Throoplast; Transit peptide.

FY TRANST 1 TRANST
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0;
  Casazza A.P., Basner A., Hoefgen R., Hesse H.;
"Expression of threonine synthase from Solanum tuberosum L. is not matabolically regulated by photosynthesis-related signals or by nitrogenous compounds.", Plant Sci. 157:43-50(2000).
-:- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threonine
  Gaps
    Gaps
  Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS). Solanum tubercsum (Potato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; Lamids; Solanales; Solanaceae; Solanum.
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  Score 48; DB 1; Length 519;
Pred. No. 15;
6; Mismatches 8; Indels
7; Indels
   2 NLWAAQRYGRELRRMSD-----EFEGSFKGL 27
   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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8; Mismatches
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   Query Match 33.6%;
Best Local Similarity 35.3%;
Matches 12; Conservative 6
8; Conservative
   STANDARD;
  [1]
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   Asteridae; lamiid
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   PubMed=10940468;
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  O9MT28;
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   Q9i9n2 brachydanio
  September 15, 2003, 17:17:131; Search time 29.3143 Seconds (without alignments) 237.680 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
  143
1 KNLWAAQRYGRELRRMSDEFEGSFKGL 27
  830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                      using sw model
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Q8VJS3
Q10843
Q10843
Q8K016
O47149
O47149
O62982
O62975
O62975
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sp_bacteria:*
sp_fungi:*
sp_fungi:*
sp_invertebrate:*
sp_nammal:*
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sp_organelle:*
  sp_vertebrate:*
sp_unclassified:*
   sp_rvirus:*
sp_bacteriap:*
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sp_rodent:*
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  sp_archeap:
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  - protein search,
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   Database
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  Result
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Gaps

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60.8%; Score 87; DB 13; Length 146; ilarity 65.2%; Pred. No. 5.9e-05; Conservative 5; Mismatches 3; Indels

Local Similarity ses 15; Conserv

Query Match Best Local S: Matches 15,

3 LWAAQRYGRELRRMSDEFEGSFK 25

δλ g 196 AA.

PRT;

PRELIMINARY;

Q8VJS3; Q8VJS3;

RESULT 2 Q8VJS3 ID Q8 AC Q8

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|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|------------|--------------------|------|------|------|------------------------------------------|------|------|--------------------|--------|--------------------|--------------|------|--------------------|--------------|--------------------|------|------|--------------------|------------------------------------------|------|--------|------|---------|--------|--------------|--------------------|-----|-------|-------------------------|--------------|--------|-----|--------------|-----------|------------------------------------|--------------------|--------|---------|-------------------------|
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| 17 52.5 36.7 18 52.5 36.7 21 52.5 36.7 22 52.5 36.7 23 52.5 36.7 24 52.5 36.7 25 52.5 36.7 26 52.5 36.7 27 52.5 36.7 28 52.5 36.7 29 52.5 36.7 29 52.5 36.7 29 52.5 36.7 31 52.5 36.7 32 52.5 36.7 33 52.5 36.7 34 52.5 36.7 35 52.5 36.7 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 39 52.5 36.7 31 52.5 36.7 31 52.5 36.7 32 52.5 36.7 34 52.5 36.7 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 39 52.5 36.7 39 52.5 36.7 30 52.5 36.7 31 52.5 36.7 32 52.5 36.7 34 51.5 36.0 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52 | 0629               | 0629       | 0629               | 0471 | 0629 | 0629 | 0629                                     | 0471 | 0629 | 0000               | 0471   | O8HS               | Q8HS<br>Q8HS | Q8HS | Q8HS<br>OBHS       | QBHS<br>QBHS | OBHS               | 0629 | 0629 | 082                | 0471                                     | SH8Ö | Æ      |      | PR      |        | Crea         | Last               |     |       | 3; E                    | Tel          |        |     | 91773        |           | nalia                              | 0(200              |        |         |                         |
| 17 52.5 36.7 18 52.5 36.7 21 52.5 36.7 22 52.5 36.7 23 52.5 36.7 24 52.5 36.7 25 52.5 36.7 26 52.5 36.7 27 52.5 36.7 28 52.5 36.7 29 52.5 36.7 29 52.5 36.7 29 52.5 36.7 31 52.5 36.7 32 52.5 36.7 33 52.5 36.7 34 52.5 36.7 35 52.5 36.7 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 39 52.5 36.7 31 52.5 36.7 31 52.5 36.7 32 52.5 36.7 34 52.5 36.7 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 39 52.5 36.7 39 52.5 36.7 30 52.5 36.7 31 52.5 36.7 32 52.5 36.7 34 51.5 36.0 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52 | 00                 | 00         | 2ο α               | သ    | 8    | သင   | ο œ                                      | 8    | ω (  | ρα                 | , ω    | တင                 | ာထ           | œ    | α α                | ω            | <b>ω</b> ο         | οα   | ο α  | 17                 | ထာထ                                      | ω    |        |      |         |        | 15,          | 22,                |     | 4     | dati                    | gii          |        |     | =10          |           | mam                                | -51                |        | pa'     | S<br>O                  |
| 17 52.5 36.7 18 52.5 36.7 21 52.5 36.7 22 52.5 36.7 23 52.5 36.7 24 52.5 36.7 25 52.5 36.7 26 52.5 36.7 27 52.5 36.7 28 52.5 36.7 29 52.5 36.7 29 52.5 36.7 29 52.5 36.7 31 52.5 36.7 32 52.5 36.7 33 52.5 36.7 34 52.5 36.7 35 52.5 36.7 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 39 52.5 36.7 31 52.5 36.7 31 52.5 36.7 32 52.5 36.7 34 52.5 36.7 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 39 52.5 36.7 39 52.5 36.7 30 52.5 36.7 31 52.5 36.7 32 52.5 36.7 34 51.5 36.0 36 52.5 36.7 37 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52.5 36.7 38 52 | 506                | 506        | 506<br>706         | 206  | 506  | 506  | 200                                      | 506  | 506  | 200                | 506    | 506                | 200          | 506  | 506                | 506          | 506                | 507  | 508  | 471                | 506                                      | 206  |        |      | MINARY; |        | Birel.       | Sirel.             |     | 1 - 1 | (Lebia<br>1; Chor       | eoptery      |        |     | PubMed       | .;<br>G.; | ogy to                             | . 7:509<br>AF66962 | ٦.     | 0616-1; | †c9⊺ ;                  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 7                  | 1          |                    |      |      | - 1  | -  -                                     | 7    | r 1  | - (                |        | <u>ر</u> . ر       |              | .7   |                    | . 1.         | r. r               | - 1- |      | 4.                 | 0.0                                      | 0.   |        |      | (ELI)   |        | TEM          | FEM                |     |       | azoi.                   | ž            | 55;    |     | N. A.        | nez       | omo I (                            | fer                | 165    | 00 6    | A.A.                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 36                 | 36         | 20 00              | 3 8  | 36   | m c  | 9 6                                      | 36   | 36   | 2 %                | 36     | 36                 | 2 %          | 36   | 8 8                | 3 6          | 36                 | 9 6  | 'n   | 36                 | W W                                      | , m  |        |      | PI      |        | -            | _                  |     |       | Met                     | ygii         | 7967=  |     | 3737         | ž.        | 적 .<br>덕 :                         | ,<br>1017          | 34;    | GENI    | 74                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 'n                 | r.         | v. r               | . 2. | ι.   | υ'n  | u.                                       | ٦.   | ı.   | o re               | . 1.   | ι.                 | 0.10         | 'n.  | κi κ               | . r.         | r, r               |      |      | 22                 | ທຸດ                                      | າທ   |        |      |         |        | 200          | 200                |     | 1     | ta;                     | ter          | XID    |     | = 20<br>= 20 | z         | wit<br>sh                          | ath<br>F23         | 929    | -BG     | Ħ                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 52                 | 52         | 2 0.0              | 52   | 52   | 22.0 | 5 2                                      | 52   | 52   | U (C               | 52     | 2.0                | U IO         | 52   | 5 E                | 52           | 52                 | J 7. | 52   |                    | 51                                       | 51   |        | Н    | 919N2   | 919N2; | 1-0CT-       | 1-0CI-             | åd. | B.    | karyc                   | ctinop       | YPL TO | 1   | SOUENC       | nohara    | Senes                              | ell De             | SSP; C | FIN; 2  | EQUENC                  |
| S S B B B B B B B B B B B B B B B B B B                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 17                 | 18         | 9 5                | 21   | 22   | 233  | 2 4                                      | 26   | 27   | 9 0                | 30     | 31                 | 3 E          | 34   | 3 3<br>3 3<br>3 4  | 37           | & c<br>(c)         | 40   | 41   | 42                 | 43                                       | 45   |        | TIDE | -       |        | 000          | 0                  | йi  | nă á  | ជ់ធ៌                    | ă ĉ          | צׁינ   | انت | 'nΣ          | H:        | . 1                                | ič 🖾               | Ħ      | Z [Z    | ń                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                    |            |                    |      |      |      |                                          |      |      |                    |        |                    |              |      |                    |              |                    |      |      |                    |                                          |      |        | RES  | įД      | AC     | 둞 돈          | i E                | E   | Z (   | 88                      | 88           | 38     | RN  | 꽃 쫎          | RA        | ER E                               | R R                | DR     | DR.     | Š                       |

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{\bf B} {\bf Y}
  Gaps
  Gaps
   INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.

EMBL; U61331; AAC15245.2; -.

Interpro; IPR000442; Intron_maturse2.
   Chloroplast.

Bukaryock; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Menziesia, NCBL_TaxID-49154;
   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rođentia, Sciurognathi, Muridae, Murinae, Mus.
  "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  .;
0
  .;
0
  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K) (Fragment).
   Score 53; DB 11; Length 946;
Pred. No. 48;
5; Mismatches 12; Indele
  Indels
  Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL. BCO34341, AAH34341.1;
Interpro; IPRO06587; VIT.
Interpro; IPRO06587; VIT.
Interpro; IPRO00235; VWR_A.
SWART; SM00327; VWR, I.
SWART; SM00327; VWR, I.
  946 AA; 105945 MW; 8B17DBA71B85BC5C CRC64;
  01-0CT-2002 (TIEMBLIEL. 22, Last sequence update) 01-MAR-2003 (TIEMBLIEL. 23, Last annotation update) Inter-alpha trypsin inhibitor, heavy chain 2.
  9:
   505 AA.
  946 AA
  Mismatches
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  37.1%; Score 53; 34.6%; Pred. No.
  2 NLWAAQRYGRELRRMSDEFEGSFKGL 27
  047148;
01-JUN-1998 (TrEMBLrel. 06, Created)
  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequ
   PRT;
  PRT;
  Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; MatK_N; 1.
   181
   18
  |||||| || | : | | |
165 NLWAADRYNRAIARGHD
   2 NLWAAQRYGRELRRMSD
  PROSITE; PS50234; VWFA; 1. SEQUENCE 946 AA: 105945
  Query Match
Best Local Similarity 34.6'
Matches 9; Conservative
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  PRELIMINARY;
   Menziesia ciliicalyx.
  [1]
SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
  TISSUE-Liver;
  10;
  Kron K.A.;
  Q8K016
Q8K016;
  047148
   ITIHZ.
  Matches
   RESULT 5
   RESULT 4
  Q8K016
  δŏ
   a
  g
   δŽ
   ö
   STRAIN-CDC 1551 / Oshkosh;
Peterschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Bolcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
   MEDLINE-9829597; PubMed-9634230; Garnier T., Churcher C., Harris D., Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Geeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., McCopering the biology of Mycobacterium tuberculosis from the
   Gaps
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  Mycobacterium tuberculosis.

Bacterias Actinobacterias Actinobacteridae, Actinomycetales, Corynebacteriaes, Mycobacteriaees Mycobacteriaeeae, Mycobacterium.

NCBL_TAXID=1773;
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
  Length 223;
   37.1%; Score 53; DB 16; Length 196; 58.8%; Pred. No. 8.4;
   6; Indels
   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007058; AAK46348.1; ''IGR: WI2070; '
   InterPro; IPR003346; Transposase_20.

Pfam; PF02371; Transposase_20; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 223 AA; 24132 MW; 70456750017EEF37 CRC64;
  Pfam; PF02371; Transposase_20; 1.
SEQUENCE 196 AA; 21349 MW; C145A8DB36FD9C2D CRC64;
   Last sequence update)
Last annotation update)
01-MAR-2002 (TIEMBLIEL. 20, Created)
01-MAR-2002 (TIEMBLIEL. 20, Last sequence update)
01-JUN-2002 (TIEMBLIEL. 21, Last annotation update)
  Score 53; DB 16;
Pred. No. 9.7;
   complete genome sequence.";
Nature 393:537-544(1998).
-!- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
  223 AA.
   Mismatches
  InterPro; IPR003346; Transposase_20.
  Created)
  PRT;
   1;
   ||||| || || || || 134 NEWAADRYNRAIARGHD 150
   2 NLWAAQRYGRELRRMSD 18
   37.1%;
   EMBL; 274025; CAA98415.1; -.
   01-NOV-1998 (TEMBLRel. 08, 01-NOV-1998 (TEMBLRel. 08, NOV-1998 (TEMBLRel. 20, Hypothetical protein RV2014, OR MTCY39,03C.
   Mycobacterium tuberculosis.
   Query Match
Best Local Similarity 58.88
Matches 10; Conservative
  PRELIMINARY;
   Tuberculist; Rv2014;
   IS1607, transposase.
   Query Match
Best Local Similarity
  SEQUENCE FROM N.A. STRAIN=H37Rv;
  SEQUENCE FROM N.A.
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Indels

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SEQUENCE Query Match

Matches

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"Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY:
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
  -:- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II INTRONS (BY SIMILARITY).
-: SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.
  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Asteridae, Ericales, Ericaceae, Ericoideae, Rhodoreae, Rhododendron.
   [1]
SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
  DB 8; Length 506;
   Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01844; MatK, M; 1.
SEQUENCE 506 AA, 60485 WW; 8A6353BFC5F4DC85 CRC64;
  DE0C07AEE608B787 CRC64;
   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Maturase K).
   | :||| : || | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  DB
  391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   506 AA.
   506 AA.
   5; Mismatches
   36.7%; Score 52.5; 37.5%; Pred. No. 28;
   5; Mismatches
   Score 52.5;
Pred. No. 28;
  EMBL; AB012749; BAA25870.1; -
EMBL; AB012745; BAA25866.1; -
Interpro; IPR000442; Intron_maturse2.
Interpro; IPR0002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N: 1.
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
   Created)
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SEQUENCE 506 AA; 60389 MW;
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37.5%;
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01-AUG-1998 (TrEMBLrel. 07,
  Rhododendron tashiroi, and Rhododendron farrerae.
  Local Similarity 37.5
nes 12; Conservative
  Query Match 36.7
Best Local Similarity 37.5
Matches 12; Conservative
   PRELIMINARY;
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  NCBI_TaxID=75582, 75580;
  J. Jpn. Bot. 0:0-0(1998)
   MATK OR YCF14.
   Chloroplast.
   SEQUENCE
  Query Match
   063960;
   062982
   098890
   Matches
  RESULT 9
O62982
   RESULT 8
   063960
  DDT TO THE READ TO THE READ TO THE READ TO THE READ TO THE READ TO THE READ TO THE READ TO THE READ TO THE READ TO THE READ THE READ TO THE READ THE READ TO THE READ TO THE READ TO THE READ TO THE READ TO THE R
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   INTROCES (BY SIMILARITY)
-!- SIMILARITY: WITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL; U61332, AAB93753.1;
  Gaps
   Gaps
   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.NCBI_TaxID=49167;
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Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
  Kron K.A.;
"Phylogenetics of Rhododendroideae (Ericaceae).";
submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  7;
  7:
   DB 8; Length 506;
   Length 505;
  Indels
   Indels
   0009EA88CD28549F CRC64;
  60233 MW; EE5F927AD2E57DE5 CRC64;
  01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
   01-JUN-1998 (TIEMBLRel. 06, Last sequence update) 01-OCT-2002 (TIEMBLRel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
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   DB 8;
   390 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 421
  1 KNLWAA------QRYGRELRRMSDEFEGSFK 25
   1 KNLWAA------QRYGRELRRMSDEFEGSFK 25
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  36.7%; Score 52.5; 37.5%; Pred. No. 28;
   Score 52.5; Pred. No. 28;
  5; Mismatches
   InterPro; IPR000442; Intron_maturse2. InterPro; IPR002866; Matk_N.
  01-00N-1998 (TrEMBLrel. 06, Created) 01-00N-1998 (TrEMBLrel. 06, Last sequ 01-0CT-2002 (TrEMBLrel. 22, Last ann
   Created)
   PRT;
   PRT;
  Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
   mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60502 MW;
  mRNA processing; Chloroplast.
  36.7%;
37.5%;
   01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
   Query Match
Best Local Similarity 37.35
These 12; Conservative
   Rhododendron edgeworthii.
   Local Similarity 37.5
nes 12; Conservative
  PRELIMINARY;
   PRELIMINARY;
   Rhododendron kiusianum.
   505 AA;
   [1]
SEQUENCE FROM N.A.
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  NCBI_TaxID=49162;
  Chloroplast.
  Chloroplast.
   Kron K.A.;
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Gaps

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8; Length 506; Indels

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RESULT 7

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Gaps

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Rhododendron (Ericaceae) based on matk Sequences.";
1. Jon. Bot. 0:0-0(1998).
1. PUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
1- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITCHONORIAL INTRON.
EMBL; AB012729; BAA25850.1; -.
InterPro: IPR00442; Intron.maturse2.
Interpro: IPR00442; Intron.maturse2.
Pfam; PF01824; Matk.N; 1.
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  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.NCBI_TaxID=75581;
  7;
  7;
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Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
   Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
  DB 8; Length 506;
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  Indels
  Indels
  "Investigation of Sectional Relationships in the Genus
  D230E54B8C20FEF0 CRC64;
  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosomal maturase (Intron maturase) (Waturase K).
  01-AUG-1998 (TrENBLrel. 07, Last sequence update) 01-OCT-2002 (TrENBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
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  | :||| : || | | 391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
                    DB
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   506 AA.
   506 AA
                  Score 52.5; Di
Pred. No. 28;
5; Mismatches
  Mismatches
   Pred. No. 28;
  Score 52.5;
  01-AUG-1998 (TrEMBLrel. 07, Created)
   PRT;
   PRT;
   36.7%; Scor.
37.5%; Pred
5; }
     36.7%; Scor.
37.5%; Pred
5; }
  506 AA; 60493 MW;
  Chloroplast,
   Local Similarity 37.5
les 12; Conservative
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   PRELIMINARY;
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Best Local Similarity
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  mRNA processing;
   Chloroplast.
   Chloroplast.
   SEQUENCE
  Query Match
   062972;
   062989
   062972
  Matches
   RESULT 12
   RESULT 11
  062989
  062972
   δŏ
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   Yukawa T;

Yukawa T;

Investigation of Sectional Relationships in the Genus
Rhododendron(Ericaceae) based on matK Sequences.";

J. Jpn. Bot. 0:0-0(1998).

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATORASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS
EMBL; AB012739; BAA25860.1;

InterPro; IPR000442; Intro.maturse2.

InterPro; IPR002866; MatK.N.
   ΒY
  Gaps
   INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
  Chilologias, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Stermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
  Rhododenáron(Ericaceae) based on matK Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
  7;
   SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
  Score 52.5'; DB 8; Length 506; Pred. No. 28;
   SEQUENCE FROM N.A.

Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi
Yukawa T.;
  Indels
  EMBL, AB012732; BAA25853.1; -.
InterPro; IPR000442; Intron_maturse2.
Interpro; IPR002866; Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N: 1.
mRNA processing; Chloroplast.
SEQUENCE 506 AA; 60449 MW; 21DFF700B071B5B8 CRC64;
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01-AUG-1998 (TremBirel. 07, Last sequence update)
01-OCT-2002 (TremBirel. 22, Last annotation update)
01-AUG-1998 (TIEMBLIEL. 07, Last sequence update) 01-OCT-2002 (TIEMBLIEL. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
  8;
   Ribosomal maturase (Intron maturase) (Maturase K)
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
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5; Mismatches
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  Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
  Chloroplast.
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37.5%;
  Query Match
Best Local Similarity 37.5'
Matches 12; Conservative
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   506 AA;
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  mRNA processing;
SEQUENCE 506 AP
  NCBI_TaxID=49628
   Chloroplast
   Chloroplast
   062975
   RESULT 10
062975
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INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MIYOCHONDRIAL INTRON
  INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
  Chloroplast.
Brkaryords, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
  Eukaryophyta; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron. NCBL_TaxID=49170;
   "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
   "Phylogenetics of Rhododendroideae (Ericaceae).";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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   855FDBDB8A5F800D CRC64;
   01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Ribosomal maturase (Intron maturase) (Maturase K).
                    (TrEMBLrel. 06, Last sequence update) (TrEMBLrel. 22, Last annotation update)
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Pred. No. 28;
   Score 52.5;
   Pred. No.
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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Interpro; IPR002866; MarK_N.
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   Chloroplast.
  Chloroplast.
A; 60439 MW;
   36.7%;
37.5%;
   36.7%;
37.5%;
   01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
(TrEMBLrel. 06, (TrEMBLrel. 06,
  Rhododendron hongkongense.
   Best Local Similarity 37.5
Matches 12; Conservative
   PRELIMINARY;
  Rhododendron tomentosum.
  mRNA processing; Ch
SEQUENCE 506 AA;
   mRNA processing; Ch
SEQUENCE 506 AA:
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Best Local Similarity
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   SEQUENCE FROM N.A.
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                    01-JUN-1998
  01-0CT-2002
  Chloroplast
   Kron K.A.;
   Kron K.A.;
   Query Match
   047152
  RESULT 15
047152
  QQ
   94
  ï
                Rhododendron(Ericaceae) based on matk Sequences.";
J. Jpn. Bot. 0:0-0(1998).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
  BY
  Gaps
  Gaps
  Chloroplast.
Bukaryocka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Asteridae; Ericales; Ericaceae; Ericoideae; Rhodoreae; Rhododendron.
   Rhododendron(Ericaceae) based on matk Sequences.";
J. Jpn. bbt. 0:0-0(1998).
-- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
--: SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
  7;
  7;
   SEQUENCE FROM N.A.
Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
Yukawa T.;
   Length 506;
  DB 8; Length 506;
  Indels
  Indels
   "Investigation of Sectional Relationships in the Genus
  "Investigation of Sectional Relationships in the Genus
   6D38A1D4D6FEC9BF CRC64;
   60350 MW; 5E832589ED64EA25 CRC64;
   Last sequence update)
Last annotation update)
  Ribosomal maturase (Intron maturase) (Maturase K) MATK.
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   DB 8;
  391 KPVWAALSDSDIIERFGRIYRNLSHYYSGSLK 422
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
  1 KNLWAA-----QRYGRELRRMSDEFEGSFK 25
   506 AA.
   506 AA.
  36.7%; Score 52.5; D
37.5%; Pred. No. 28;
iive 5; Mismatches
  5; Mismatches
   Score 52.5; |
Pred. No. 28;
  EMBL, AB012735, BAA25856.1, -
InterPro, IPR000442; Intron_maturse2.
InterPro, IPR002866; MatK_N.
  MITOCHONDRIAL INTRONS.
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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   Pfam; PF01348; Intron_maturas2; 1. 
Pfam; PF01824; Matk_N; 1.
   Pfam; PF01348; Intron_maturas2; 1.
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   36.7%;
37.5%;
   Pfam, PF01824; Matk_N; 1.
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SEQUENCE 506 AA; 60350 MW;
  ilarity 37.5%;
Conservative
   01-AUG-1998 (TrEMBLrel. 07, 01-OCT-2002 (TrEMBLrel. 22,
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   PRELIMINARY;
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  Best_Local Similarity
Matches 12; Conserv
  Similarity
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  12;
   SEQUENCE
   Query Match
Best Local S
  Query Match
   047155
   062978
  Matches
   RESULT 14
   RESULT 13
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047155 ID 04

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Gaps

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Indels

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7; Gaps

8; Indels 1 KNLWAA------GRYGRELRRWSDEFBGSFK 25 | :|| | :|| | :|| | 391 KPVWAALSDSDIJERFGRIYRNLSHYYGGSLK 422 Matches 12; Conservative 5; Mismatches Search completed: September 15, 2003, 17:25:50 Job time : 29.3143 secs Db QY

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10
  September 15, 2003, 17:16:01; Search time 22.6286 Seconds (without alignments) 112.231 Million cell updates/sec
  1107863
                                     Compugen Ltd.
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
  Total number of hits satisfying chosen parameters:
  1107863 segs, 158726573 residues
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   OM protein - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   1 QRYGRELRRMSDEFEG (16)
   Minimum DB seq length: 0 Maximum DB seq length: 20000000000
  US-09-544-664-28
84
   Scoring table:
   Perfect score:
  Searched:
   Sequence:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| UMMARIES |  |
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| Description                   | Mouse BAD BH3 doma | Bcl2 polypeptide B | bcl-x(L)/bcl-2 ass | Bcl2 polypeptide B | Bcl2 polypeptide B | Bcl2 polypeptide B | Bcl2 polypeptide B | Bcl2 polypeptide B | Shorter murine BAD |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| a                             | AAY05422           | AAB37028           | AAR95166           | AAB37001           | AAB37002           | AAB37003           | AAB37056           | AAB37055           | AAB70370           |
|                               | 20                 | 21                 | 17                 | 21                 | 21                 | 21                 | 21                 | 21                 | 22                 |
| %<br>Query<br>Match Length DB | 16                 | 16                 | 23                 | 26                 | 26                 | 27                 | 27                 | 28                 | 162                |
| %<br>Query<br>Match ]         | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              |
| Score                         | 84                 | 84                 | 84                 | 84                 | 84                 | 84                 | 84                 | 84                 | 84                 |
| Result No.                    | 1                  | 7                  | m                  | 4                  | Ŋ                  | 9                  | 7                  | 8                  | 6                  |

| L)/bc<br>BCL-<br>BCL-<br>BCL-<br>BCL-<br>BCL-<br>BAD<br>muri         |                                                                                   | Bad pe<br>Bad pe<br>Bad pe<br>Bad pe<br>Bad pe                       | Bad pe<br>Bad pe<br>Bad pe<br>nterac<br>Bcl2 f<br>Bcl2 f<br>Bcl2 f               | Mutant Boll Compet<br>Mutant Boll Compet |
|----------------------------------------------------------------------|-----------------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AAR95168<br>AAW61315<br>AAW61316<br>AAW61317<br>AAW61318<br>AAB70369 | ABR39082<br>AAU00220<br>AAX376421<br>AAB37029<br>ABG78483<br>AAU78609<br>ARG78493 | AAU78626<br>ABG78500<br>AAU78608<br>AAU78630<br>AAU78629<br>AAU78629 | AAU78605<br>AAU78627<br>AAU78627<br>ABP56161<br>ABG78481<br>ABG78484<br>ABG78485 | ABG78487<br>ABG78489<br>ABG78490<br>ABG78491<br>ABG78491<br>ABG78492<br>ABG78492                                                                                                                   |
| 110<br>110<br>110<br>110<br>110<br>110                               | 222222<br>222222                                                                  | 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7                              | 22222222                                                                         | 999999999                                                                                                                                                                                          |
| 24444444444444444444444444444444444444                               | 094446                                                                            | 000000000000000000000000000000000000000                              | 4 4 4 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3                                          | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                              |
|                                                                      |                                                                                   |                                                                      |                                                                                  | $\begin{smallmatrix} \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha $                                                                                     |
| \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$             | 4884<br>733<br>733<br>733<br>733                                                  | 773333                                                               |                                                                                  | 27 7 7 7 7 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                           |
| 10<br>11<br>12<br>14<br>14<br>15                                     | 17<br>18<br>20<br>21<br>23<br>23                                                  | 10000000<br>10000000000000000000000000000                            | )                                                                                | Დ Ნ Ტ ᠳ 전 전 전 전 전                                                                                                                                                                                  |

## ALIGNMENTS

AAY05422 standard; peptide; 16 AA (first entry) 02-JUL-1999 AAY05422; AAY 05422

RESULT 1

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*

A\_Geneseq\_19Jun03:\*

Database :

BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptiosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer: lymphoprollferative condition; arthritis; autoimmune disease; therapy. Mouse BAD BH3 domain. 

Mus sp

(0) (e) (1 km ft. tr. 10) 98WO-US19765. W09916787-A1 22-SEP-1998; 08-APR-199\$.

97US-0946039. 07-OCT-1997; 26-SEP-1997;

Korsmeyer SJ;

(UNIW ) UNIV WASHINGTON

WPI; 1999-255058/21.

a

us-09-544-664-28.rag

```
Korsmeyer SJ;
  WO9613614-A1.
  Mus musculus.
   31-OCT-1995;
   31-OCT-1994;
  03-JAN-1997
   09-MAY-1996.
   Sequence
  AAR95166;
   Query Match
   Best Loc
Matches
  RESULT 3
   AAR95166
  8888888888888888888888888888888888
  δλ
  g
   ő
  This sequence represents the BH3 domain of mouse BAD.

The invention relates to a bc1 homology domain 3 (BH3 domain),
derived from a prosportic member of the BCL-2 family. The
BH3 polypeptide can be used in a method for promoting apoptosis in a
target cell, especially where the cell is a cencer cell a virus infected
cell or an autoantibody producing cell. The BH3 polypeptide can be used
in therapeutic compositions for treating disease including cancer, other
lymphoproliferative conditions, arthritis, inflammation, and autoimmune
diseases, which may result from the down regulation of cell death
  The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X=0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain functional group is C=10 or C=110 or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
  Gaps
  Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
   New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
   0;
  Length 16;
   0; Indels
  100.0%; Score 84; DB 20;
100.0%; Pred. No. 2.6e-07;
iive 0; Mismatches 0;
   Lu Z;
   Bcl2 polypeptide BH3 domain peptide #28.
   Huang Z, Wang J, Zhang Z, Shan S,
   AAB37028 standard; peptide; 16 AA.
Bcl homology domain 3 polypeptide
  Claim 18; Page 18; 74pp; English.
                                      Example 1; Fig 4; 104pp; English.
  (UYJE-) UNIV JEFFERSON THOMAS.
   1 ORYGRELRRMSDEFEG 16
  1 ORYGRELRRANSDEFEG 16
  06-APR-2000; 2000WO-US09352.
  99US-0128202.
   (first entry)
   Conservative
   WPI; 2000-679325/66.
  Local Similarity
nes 16; Conserv
  16 AA;
  WO200059526-A1.
   Homo sapiens.
  07-APR-1999;
   28-FEB-2001
  12-OCT-2000.
  requlation.
  Sequence
   AAB37028;
  Query Match
   Matches
  RESULT 2
```

П

g δ

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monosubstituted with a 1-5C straight or branched chain alkyl group,

phenyl optionally monosubstituted with a 1-5C straight or branched chain

alkyl group, or benzyl. The peptides ABB37001-B37058 represent examples

of the peptide portion of the conjugate. The peptides represent analogues

of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

the BH3 domain of the cell death agonist Bad. The peptide conjugate is

useful for modulating apoptosis in the cells of a subject, or for

reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of

apoptosis in cancer cells. It is also useful for inhibiting Bcl-2

tunction. In particular, the peptide conjugate is useful for treating a

cute tafflicted with a cancer characterized by cancer cells that

express Bcl-2. The cancer includes prostate, colorectal, gastric,

non-small lung, renal or thyroid cancers, neuroblastoma, melanoma,

cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

conjugate is also useful for treating disorders characterized by

increased apoptosis, eg, neurodegenezative disorders, acquired

immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BHI; BH3, appitotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AlDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
  The sequences given in AAR95155-67 represent epitopes derived from the murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death
   Gaps
  Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers
   bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.
   ·
0
  100.0%; Score 84; DB 21; Length 16; 100.0%; Pred. No. 2.6e-07;
  Indels
   Mismatches
  Claim 2; Page 103; 130pp; English.
  AA.
  0;
   AAR95166 standard; peptide; 23
   1 ORYGRELRRMSDEFEG 16
   1 ORYGRELRRMSDEFEG 16
   94US-0333565.
   95WO-US14246.
   (first entry)
  Conservative
  (UNIW ) UNIV WASHINGTON.
  WPI; 1996-251465/25.
   Local Similarity
wes 16; Conserv
   16 AA;
```

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ö
inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptoric cell death induced by ytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L) and may be used to identify agents which inhibit it its binding to bcl-x(L) or bcl-x(L) to form heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
   The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH; when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy. 2-14C alkylenyl containing one or two double bonds, cyclobuttyl, cyclopentyl, cyclopentyl containing one or two double bonds, cyclobuttyl, cyclopentyl, cyclopentyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides Aba37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72.97 of
  Gaps
   New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/Jeukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
  .;
0
  Length 23;
  0; Indels
  Score 84; DB 17;
Pred. No. 3.7e-07;
   : 2
  Mismatches
   Γŗ
  Bcl2 polypeptide BH3 domain peptide #1.
   Huang Z, Wang J, Zhang Z, Shan S,
   AAB37001 standard; peptide; 26 AA.
   Claim 18; Page 17; 74pp; English.
  ·,
   (UYJE-) UNIV JEFFERSON THOMAS.
  100.0%;
   100.0%;
   1 ORYGRELRRMSDEFEG 16
   06-APR-2000; 2000WO-US09352.
   99US-0128202.
   (first entry)
  16; Conservative
  senescence or ischaemia.
   WPI; 2000-679325/66.
  Query Match
Best Local Similarity
  23 AA;
   WO200059526-A1.
   28-FEB-2001
   07-APR-1999;
   Homo sapiens
   12-OCT-2000
  Sequence
  Matches
   RESULT 4
        88888888888
  ŏ
  셤.
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The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C-6, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group is of the side chain is NH2 or OH; or X=0 or NH4, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R=2-16C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain
           useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject affilicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for treating also consectal and non-lymphocytic leukemia. The peptide increased apoptosis, e.g. neurodogenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 peptide conjugate is
  Gaps
   ω
   Cytostatic; neuroprotective; anti-HIV; virudide; cerebroprotective; cardiant; Bcl_2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/levemia 2; cancer; prostate; colorectal; gastric; nor-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
   New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  0;
  Length 26;
  Indels
  100.0%; Score 84; DB 21; 100.0%; Pred. No. 4.2e-07;
  ö
   2
  Mismatches
   n
   Bcl2 polypeptide BH3 domain peptide #2.
   Shan S,
   AA.
  Claim 18; Page 17; 74pp; English.
  0;
   AAB37002 standard; peptide; 26
  stroke; myocardial infarction.
   (UYJE-) UNIV JEFFERSON THOMAS.
  16
  ORYGRELRRMSDEFEG 21
   Zhang Z,
   06-APR-2000; 2000WO-US09352
   99US-0128202
   (first entry)
  1 ORYGRELRRMSDEFEG
  Local Similarity 100. tes 16; Conservative
   WPI; 2000-679325/66.
   Wang J,
  26 AA;
  WO200059526-Al.
  Homo sapiens.
   07-APR-1999;
   28-FEB-2001
  12-0CT-2000
   AAB37002;
   Huang Z,
  Sequence
  Query Match
  Matches
   RESULT 5
   AAB37002
   55555555555555
  QΫ
  g
```

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alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for eversing B cell lymphoma/leukemia 2 (Bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bc1-2 function. In particular, the peptide conjugate is useful for treating a subject affilicted with a cancer characterized by cancer cells that express Bc1-2. The cancer includes prostate, colorectal, gastric, on small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   ó
  The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; x = c=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or x = 0 or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, or a side chain of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
   Gaps
  New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bol.2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/Jeukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma.
   melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
   0;
  Length 26;
   Indels
   .
0
  Score 84; DB 21;
Pred. No. 4.2e-07;
   Mismatches
  Ę
   Bcl2 polypeptide BH3 domain peptide #3.
  Huang Z, Wang J, Zhang Z, Shan S,
   AAB37003 standard; peptide; 27 AA.
   Claim 18; Page 17; 74pp; English.
   ;
0
   100.0%;
  (UYJE-) UNIV JEFFERSON THOMAS.
   stroke; myocardial infarction
  1 ORYGRELRRMSDEFEG 16
  ORYGRELRRMSDEFEG 21
  06-APR-2000; 2000WO-US09352.
   99US-0128202.
  (first entry)
   Query Match 100.

Best Local Similarity 100.
Matches 16; Conservative
   WPI; 2000-679325/66.
  26 AA;
   WO200059526-A1.
  28-FEB-2001
  Homo sapiens
   07-APR-1999;
   12-OCT-2000.
  Sequence
   ω
   AAB37003;
  cell
  RESULT 6
  AAB37003
  8599999999999999999988888
   셤
  QΩ
```

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or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides Aps37001-B37058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for eversing B cell lymphomal-lenkemia 2 (Bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bc1-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bc1-2. The cancer includes prostate, colorectal, gastric, con-amal lung, renal or thyroid cancers, neuroblastoma, melanoma, or cancer chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders characterized by immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
  The invention relates to a peptide conjugate having the formula: (x,x)n-repetide where n = 1-10, x = C=0, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NHZ or OH; or X = 0 or NH,
   Gaps
   œ
  Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
   New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
   ٠<u>;</u>
  Length 27;
   Indels
  treating neurodegenerative disorders, stroke, or cancer
   .
0
  100.0%; Score 84; DB 21; 100.0%; Pred. No. 4.4e-07;
   7
   Mismatches
   3
   Bcl2 polypeptide BH3 domain peptide #56.
   'n
   Shan
  AAB37056 standard; peptide; 27 AA.
   Claim 18; Page 19; 74pp; English.
   0;
  (UYJE-) UNIV JEFFERSON THOMAS.
  1 ORYGRELRRMSDEFEG 16
   2
   Zhang Z,
  06-APR-2000; 2000WO-US09352.
   99US-0128202.
  28-FEB-2001 (first entry)
   6 ORYGRELRRMSDEFEG
   Local Similarity 100.
nes 16; Conservative
  WPI; 2000-679325/66.
   Wang J,
   27 AA;
  WO200059526-A1.
   Homo sapiens.
   07-APR-1999;
   12-OCT-2000.
   AAB37056;
   Huang Z,
   Sequence
  Query Match
   Best Loc
Matches
   RESULT 7
   AAB37056
  g
        ã
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when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONHE; and R = 2-18¢ alkyla calkxyy, 2-16¢ alkylaryl contabiling one or two double bonds, cyclobutyl, cyclopeatyl, cyclohexyl optionally monosubstituted with a 1-5¢ straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5¢ straight or branched chain alkyl group, or benzyl. The peptides ABA37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptides conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphomal-deukemla 2 (Bcl-2)-mediated blockage of reversing B cell lymphomal-deukemla 2 (Bcl-2)-mediated blockage of reversing B cell lymphomal-deukemla 2 (Bcl-2)-mediated blockage of subject sit cancer cells in the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that cancer includes prostate, colorectal, gastic, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   ·;
   Gaps
  Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; BG1-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
  New peptide conjugates for modulating apoptosis or for inhibiting B
  cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  The invention relates to a peptide conjugate having the formula:
   ò
  Score 84; DB 21; Length 27; Pred. No. 4.4e-07;
   Indels
   .;
0
  7
   Mismatches
  ដូ
   Bcl2 polypeptide BH3 domain peptide #55.
  Huang Z, Wang J, Zhang Z, Shan S,
  AAB37055 standard; peptide; 28 AA.
   Claim 18; Page 19; 74pp; English.
   0;
  100.0%;
  stroke; myocardial infarction.
   (UYJE-) UNIV JEFFERSON THOMAS.
   1 ORYGRELRRMSDEFEG 16
  7 ORYGRELRRMSDEFEG 22
   06-APR-2000; 2000WO-US09352.
  99US-0128202.
  (first entry)
  Local Similarity 100.
hes 16; Conservative
   WPI; 2000-679325/66.
   27 AA;
  WO200059526-A1.
  07-APR-1999;
  28-FEB-2001
   Homo sapiens.
  12-OCT-2000.
   Sednence
   AAB37055;
  Query Match
   Matches
  RESULT 8
  AAB37055
        ğ
  qq
```

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to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OB; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide where the functional group of the side chain is NH2 or OB; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and X = 2.18¢ alf xl or alf calkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5c straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5c straight or branched chain alkyl group, or benzyl. The peptides Aba37001-B3705B represent analogues of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma-laukemia 2 (Bcl.2) mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl.2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer calls that
   0
  express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
   Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive, apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertiin; lymphoproliferative condition; inflammation; autoimmune disease.
   New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit
  increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
   .;
0
   100.0%; Score 84; DB 21; Length 28; 100.0%; Pred. No. 4.5e-07;
   Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
  Indels
  .
0
  Mismatches
   AAB70370 standard; protein; 162 AA.
   (APOP-) APOPTOSIS TECHNOLOGY INC.
  0;
   1 ORYGRELRRMSDEFEG 16
  7 QRYGRELRRMSDEFEG 22
   30-MAY-2000; 2000WO-US11864.
  99US-0136783.
  (first entry)
  16; Conservative
   WPI; 2001-138734/14.
  Local Similarity
  28 AA;
  WO200110888-A1.
   Mus musculus,
  02-MAY-2001
  28-MAY-1999;
  15-FEB-2001.
  Synthetic.
  Sequence
  Query Match
  Zhou X;
  Matches
  RESULT 9
  q
  á
```

9

us-09-544-664-28.rag

```
Korsmeyer SJ;
  Seguence
  AAW61315;
   Query Match
   Mus sp.
  RESULT 11
  QY
  (1) comprising a less than full length amino acid sequence of a mutant of 10 comprising a less than full length amino acid sequence of a mutant fragment, which contains amino acid substitutions at Serils of a human acid season at Serils of a human bab, SeriSs of a mutine BAD (longer mutine BAD) or Serils of a mutine BAD (longer mutine BAD) or Serils of a mutine DAD, (1) has immunostimulant, neuroprotective, contropic, antilischemic, vulnerary mutuostimulant, neuroprotective, antiarthritic, antiliflammatory and immunosuppressive activities, and colluctions as an apoptosis inducer or inhibitor. BAD polypeptides and polymetotides and personal series of a confound and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autolimmune diseases. The present sequence represents a specifically claimed shorter mutine BAD mutant amino acid sequence from the present
   0;
   Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease, senescence; isohaemia; neoplasia.
   Gaps
  synthetic polypeptide
apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
   0;
  Length 162;
  Score 84; DB 22; Length 1
Pred. No. 2.7e-06;
Mismatches 0; Indels
   Location/Qualifiers
147...149
/note= "BH1 conserved amino acids"
  "BH2 conserved amino acids"
   bcl-x(L)/bcl-2 associated death promoter protein.
  invention describes an isolated or
  /note= "PEST sequence"
1111.130
/note= "PEST sequence"
   Claim 7; Page 148-149; 157pp; English.
   AAR95168 standard; Protein; 204 AA.
  .;
0
  th 100.0%;
| Similarity 100.0%;
| 16; Conservative 0;
  16
   94US-0333565.
   95WO-US14246
  06-JAN-1997 (first entry)
   1 ORYGRELRRMSDEFEG
   .192
   (UNIW ) UNIV WASHINGTON.
  /note=
38..61
   Local Similarity
  162 AA;
   Mus musculus
   WO9613614-A1
   31-OCT-1995;
   31-OCT-1994;
  09-MAY-1996
  Sequence
  AAR95168;
  Query Match
  Key
Region
   Region
  Domain
  Domain
   Matches
   RESULT 10
  AAR95168
  \mathbb{Z} \times 
   δ
   qq
```

```
This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 proteins and regulates cell death. It has bomology to the bcl-2-related family clustered in the Bill and Bill domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mamalian cells. Overexpressed Bad counters the ceath inhibitory activity of bcl-x(L), but is much less effective at a conterring the death inhibitory activity of bcl-x(L), and its also counters the accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the centh repressor activity of bcl-x(L). Bad competes with bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be a block of the processing but the processing but the processing but the processing bol-x(L) and its also counters the counter of the bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be also because the bol-x(L) and block and brock  Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
   Gaps
  Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers
  New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection
   0
  100.0%; Score 84; DB 17; Length 204; 100.0%; Pred. No. 3.5e-06; O. Mismatches 0; Indels 0
  Murine BCL-XL/BCL-2 associated cell death regulator.
   e.g. AIDS, senescence or ischaemia.
  AAW61315 standard; Protein; 204 AA.
  Claim 3; Fig 1; 130pp; English.
   Claim 1; Fig 10; 95pp; English
  145 ORYGRELRRMSDEFEG 160
  1 ORYGRELRRMSDEFEG 16
   97WO-US19175.
  96US-0733505.
  (first entry)
  Best Local Similarity 100.
Matches 16; Conservative
   (UNIW ) UNIV WASHINGTON.
  WPI; 1998-261422/23.
WPI; 1996-251465/25.
  204 AA;
   N-PSDB; AAV27833
  N-PSDB; AAT29479
  Korsmeyer SJ;
  WO9817682-A1.
   17-0CT-1997;
  18-OCT-1996;
   07-0CT-1998
   30-APR-1998.
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.; 0

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infamiliaring and autoimmune disease. Polyrucideotide sequences entitle annuals for use as disease models or in first infertility or proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in fung screening. BAD proteins phosphorylated at specified sea are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, determined by measuring relative amounts of phosphorylated and nonphosphorylated BAD, by usual immunossays, Mutant BAD proteins have greater death-promotting activity than wild-type BAD brich can become phosphorylated on the specified Ser, forming a product that does not heterodiments with BCL-SL but instead binds to 14-33 family, heterodiments with BCL-SL but instead binds to 14-33 family.
   ·,
   Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
   proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
   Gaps
  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
   0;
   100.0%; Score 84; DB 19; Length 204; 100.0%; Pred. No. 3.5e-06; ive 0; Mismatches 0; Indels (
  Mutant BCL-XL/BCL-2 associated cell death regulator #1.
   AAW61316 standard; Protein; 204 AA.
   100.08; FIL
  Claim 7; Paqe 59; 95pp; English.
   145 QRYGRELRRMSDEFEG 160
  1 ORYGRELRRMSDEFEG 16
  97WO-US19175.
  96US-0733505
  07-OCT-1998 (first entry)
  Best Local Similarity 100.0
Matches 16; Conservative
   (UNIW ) UNIV WASHINGTON
  WPI; 1998-261422/23.
N-PSDB; AAV27834.
  204 AA;
   Korsmeyer SJ;
  17-0CT-1997;
   WO9817682-A1.
  18-OCT-1996;
   30-APR-1998.
  Synthetic.
   AAW61316;
  Seguence
   Query Match
   Mus
  AAW61316
  8
X888888888888888888888888888888
  δ
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death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein able to decrease cell viability, (2) fusion proteins of mutant BAD protein able to decrease cell viability, (2) increases intracellular delivery whether BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infammation and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transquant BAD proteins can be used similarly by gene therapy or to produce mutant BAD proteins can be used similarly by gene therapy or to produce ransquant animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serime-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated and not he specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family cortains in the cytosol, thus promoting cell survival. The mutants with the proteins in the cytosol, thus promoting cell survival. The mutants with the protein bind 14-3-3.
  ó
  Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
   The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
  Gaps
   New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection
  0;
  100.0%; Score 84; DB 19; Length 204; 100.0%; Pred. No. 3.5e-06;
  0; Indels
   Mutant BCL-XL/BCL-2 associated cell death regulator #2.
  0; Mismatches
   AAW61317 standard; Protein; 204 AA.
   Claim 7; Page 60; 95pp; English.
  145 QRYGRELRRMSDEFEG 160
  1 ORYGRELRRMSDEFEG 16
  97WO-US19175.
  96US-0733505
   (first entry)
  Query Match
Best Local Similarity 100.
Matches 16; Conservative
  (UNIW ) UNIV WASHINGTON.
  WPI; 1998-261422/23.
   204 AA;
   N-PSDB; AAV27835
  Korsmeyer SJ;
  17-OCT-1997;
  18-OCT-1996;
  WO9817682-A1
   07-0CT-1998
  30-APR-1998
  Mus sp.
Synthetic.
   Sednence
   AAW61317;
   RESULT 13
  AAW61317
   8888888888888888888888888888888
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  q
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presents advance represents a mutant BAD protein Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fragments of mutant BAD with a heterologous polypeptide that finish on proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, virial infection, lumphoproliferation, arthritis, infertility, infertility, infartility, or an expection be used similarly by gene therapy or to produce transgenic animals for use as disease. Polymucleotide sequences encoding proteins phosphorylated at specified Ser are used to screen for enhancers or inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, or aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays, whuch BAD proteins have composited on the specified Ser, forming a product that does not cherodismarise with BCL-2 or BCL-XL but instead binds to 14-3-3 family, between the cannot bind 14-3-3.
  ô
  Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
  The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at
death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
  Gaps
  New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
  ó
  100.0%; Score 84; DB 19; Length 204; 100.0%; Pred. No. 3.5e-06; ive 0; Mismatches 0; Indels
   Mutant BCL-XL/BCL-2 associated cell death regulator #3.
  Claim 7; Page 60-61; 95pp; English.
   AAW61318 standard; Protein; 204 AA.
  100.0%;
   1 QRYGRELRRMSDEFEG 16
   97WO-US19175.
  96US-0733505.
  (first entry)
  16; Conservative
   (UNIW ) UNIV WASHINGTON.
  WPI; 1998-261422/23.
N-PSDB; AAV27836.
  Query Match
Best Local Similarity
   204 AA;
   Korsmeyer SJ;
  WO9817682-A1.
   17-OCT-1997;
  07-0CT-1998
  18-OCT-1996;
   30-APR-1998.
  Mus sp.
Synthetic.
   Seguence
   AAW61318;
  Matches
   AAW61318
  XXXXX SSSXXXX SSXXXX SSXXXX SSXXXX SSXXXX SSXXXX SSXXXX SSXXX SXXXX XXX SXX SXXX SXX  SXX 
  9
   QΫ
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position 12 ang/or 130, relative to the mutine bab 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, Imphoprorlieration, arthritis, infertility, and an example as disease models or in furg screening and inhibitors of serine-phosphatase. Inhibitors are potentially useful to transpend of serine-phosphatase. Inhibitors are potentially useful and inhibitors of serine-phosphatase. Inhibitors are potentially useful determined by measuring relative amounts of phosphorylated and non-determined by measuring relative amounts of phosphorylated and non-phosphorylated on the specified Ser, forming a product that does not consecuence of the product in the cytosol, thus promoting cell survival. The mutants with Serial promoting cell survival. The mutants with serial promoting cell survival. The mutants with
  ö
position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
  BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease; neurodegenerative disease; infertility; cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
  Gaps
   Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
   This sequence represents a novel serine-phosphorylated protein, BAD
  0;
  Length 204;
  Score 84; DB 19; Length 2 Pred. No. 3.5e-06; Mismatches 0; Indels
   AAW58832 standard; protein; 204 AA
  .:
   100.0%;
   Claim 3; Fig 8; 61pp; English.
   1 QRYGRELRRMSDEFEG 16
   96US-0707868.
  (first entry)
   Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
   UNIW ) UNIV WASHINGTON
  WPI; 1998-207049/18.
   Murine BAD protein.
  204 AA;
   Korsmeyer SJ;
   WO9809643-A1.
  09-SEP-1997;
   09-SEP-1996;
  23-JUL-1998
   12-MAR-1998.
  Seguence
  RESULT 15
   88888888888888888888888888888888
   g
  δŽ
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CC (Bc1-X1/Bc1-2 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding cc to the 14-3-3 protein which is a signal transduction regulator.

CC of a phosphoserine phosphatase, are useful for preventing/treating cc increased/decreased apoptosis in a cell. The increased apoptosis may cresult from immunodeficiency disease, senescence, neurodegenerative disease, ischaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral cc infection, lympoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total cc bab in a cell is useful for determining the apoptotic state of a cell. XX

Query Match

Query Match

Query Match

Query Match

Ast, conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 10, Gaps 0; Indels 0; Gaps 0; In
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Search completed: September 15, 2003, 17:22:13 Job time : 22.6286 secs

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September 15, 2003, 17:22:21; Search time 8.34286 Seconds (without alignments) 81.144 Million cell updates/sec
  328717
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
  328717 segs, 42310858 residues
  using sw model
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  US-09-544-664-28
84
1 QRYGRELRRMSDEFEG 16
  OM protein - protein search,
  Title:
Perfect score:
  Scoring table:
  Searched:
  Sequence:
   Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|            | Description  |       | 10,          | 7               | 7         | H                | 12,       | 13,       | 74           | 'n        | m      | 55,            | 56,         | 57,         | 58,          | 7   | 7        |           |           | 'n           | 7            | 2            | 26,    | 26,        | 18,           | 18,       | 270       | Sequence 34, Appl |
|------------|--------------|-------|--------------|-----------------|-----------|------------------|-----------|-----------|--------------|-----------|--------|----------------|-------------|-------------|--------------|-----|----------|-----------|-----------|--------------|--------------|--------------|--------|------------|---------------|-----------|-----------|-------------------|
|            | QI           |       | -08-661-479- | US-08-333-565-2 | -661-479- | US-08-733-505A-1 | -08-733-5 | -08-733-5 | -08-733-505A | -08-717-1 | 5-257- | -08-733-505A-5 | 38-733-505A | -733-5      | -08-733-505A |     | -717-123 | -985-335- | -08-985-3 | -09-410-372- | -09-410-372- | -09-375-257- | -333-5 | -661-479-2 | -08-718-738-1 | -09-221-8 | 9-252-991 | .08-733-5         |
|            | DB           | Н     | ~            | Н               | 7         | 7                | ~         | 7         | 7            | ~         | 4      | ~              | 7           | ~           | ~            | -г  | 7        | m         | m         | e            | ო            | 4            | -      | a          | က             | m         | ₽.        | 7                 |
|            | Match Length | 23    | 23           | 204             | 204       | 204              | 204       | 204       | 204          | 204       | 204    | 59             | 59          | 9<br>0<br>0 | 59           | 166 | 168      | 168       | 168       | 168          | 168          | 168          | 16     | 16         | 213           | 213       | 591       | 11                |
| %<br>Ouerv | Match        | 100.0 |              | 00              |           | 100.0            |           |           | 100.0        | 96.4      | 96.4   |                |             |             |              |     |          |           |           |              |              |              |        |            |               |           | 51.2      |                   |
|            | Score        | 84    | 84           | 84              | 84        | 84               | 84        | 84        | 84           | 58        | 81     | 73             | 73          | 73          | 73           | 73  | 73       | 73        | 73        | 73           | 73           | 73           | 67     | 49         | 43            | 43        | 43        | 42                |
| Result     | No.          | 7     | 7            | m               | 4         | រេ               | 9         | 7         | œ            | O         | 10     | 11             | 12          | 13          | 14           | 15  | 16       | 17        | 18        | 19           | 20           | 21           | 22     | 23         | 24            | 25        | 26        | 27                |

| 42 50.0 11 2 US-08-706-741B-69<br>41 50.0 11 2 US-08-706-741B-69<br>41 40.5 48.2 90.4 4 US-09-238-312-4656<br>32 40 47.6 50.5 4 US-09-238-312-4656<br>33 46.4 33 4 US-09-238-91R-21995<br>34 46.4 33 4 US-09-52-91R-218729<br>35 46.4 33 4 US-09-52-991R-218729<br>36 45.2 112 4 US-09-52-991R-218729<br>37 44.0 125 4 US-09-52-991R-28667<br>40 37.5 44.6 90.6 4 US-09-52-991R-218667<br>41 37 44.0 125 4 US-09-252-991R-218687<br>42 44.0 125 4 US-09-252-991R-218687<br>43 44.0 125 4 US-09-252-991R-218687<br>44 41.0 143 4 US-09-252-991R-218687<br>45 46 96 4 US-09-252-991R-218687<br>46 12 12 4 US-09-252-991R-218687<br>47 48.0 125 4 US-09-252-991R-218687<br>48 4 US-09-252-991R-218687<br>49 40.0 28 4 US-09-252-991R-218687<br>40 18 18 18 18 18 18 18 18 18 18 18 18 18                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Sequence 32234, A    | Sequence 26483, A    | Sequence 6559, Ap  | Seguence 29777, A    | Sequence 7449, Ap  | Sequence 31458, A    | Seguence 26867, A    | 29351,               | Sequence 26270, A    | Sequence 27256, A    | Sequence 18729, A    | Sequence 28443, A    | Sequence 40, Appl |                      |                    |                 | Seguence 69, Appl | Sequence 69, Appl |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------|----------------------|--------------------|----------------------|--------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|-------------------|----------------------|--------------------|-----------------|-------------------|-------------------|
| 42 50.0 11<br>40.5 50.0 11<br>40.5 50.0 11<br>40.5 60.0 322<br>40.6 48.8 904<br>40.6 47.6 505<br>39.8 46.4 1125<br>38.5 46.4 1125<br>38.5 46.4 1125<br>38.5 46.4 1125<br>38.5 46.7 1125<br>38.5 46.7 1125<br>38.5 46.0 1125<br>37.5 44.6 906<br>37.5 44.0 125<br>37.7 44.0 125<br>37.7 44.0 125<br>37.8 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 44.0 125<br>37.9 | US-09-252-991A-32234 | US-09-252-991A-26483 | US-09-328-352-6559 | US-09-252-991A-29777 | US-09-328-352-7449 | US-09-252-991A-31458 | US-09-252-991A-26867 | US-09-252-991A-29351 | US-09-252-991A-26270 | US-09-252-991A-27256 | US-09-252-991A-18729 | US-09-252-991A-28443 | US-08-867-087B-40 | US-09-252-991A-21995 | US-09-328-352-4656 | US-09-359-161-7 | US-08-924-695A-69 | US-08-706-741B-69 |
| 40.00000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4                    | 4                    | 4                  | 4                    | 4                  | 4                    | 4                    | 4                    | 4                    | 4                    | 4                    | 4                    |                   | 4                    | 4                  | 4               | ~                 | 7                 |
| 0 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 309                  | 301                  | 284                | 143                  | 125                | 906                  | 670                  | 574                  | 376                  | 1112                 | 1125                 | 333                  | 99                | 505                  | 904                | 322             | 1                 | 77                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 44.0                 | 44.0                 | 44.0               | 44.0                 | 44.0               | 44.6                 | 45.2                 | 45.2                 | 45.2                 | 45.8                 | 46.4                 | 46.4                 | 46.4              | 47.6                 | 48.2               | 48.8            | 50.0              | 50.0              |
| 20000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 37                   | 37                   | 37                 | 37                   | 37                 | 37.5                 | 38                   | 38                   | 38                   | 38.5                 | 39                   | 39                   | 39                | 40                   | 40.5               | 41              | 42                | 42                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ر<br>ا               | 44                   | 43                 | 42                   | 41                 | 40                   | ه<br>8               | 38                   | 37                   | 36                   | 32                   | 34                   | 33                | 32                   | 31                 | 30              | 29                | 28                |

ALIGNMENTS

|  | RESULT 1 US-08-333-565-10 Sequence 10, Application US/08333565 Sequence 10, Application US/08333565 Patent No. 5522832 GENERAL INFORMATION: APPLICANT: KORNEYER, Stanley J. TITLE OF INVENTION: BC1-x/BC1-2 ASSOCIATED CELL DEATH TITLE OF INVENTION: REGULATOR NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: ADDRESSER: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STAME: California COUNTRY: US TIP: 94301 COMPUTER: IBM PC compatible COUNTRY: US OFFEATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: PETACHIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/333,565 FILING DATE: 31-CC-194 CLASSIFICATION: 435 ATTORREY-CONCET WINDER: 30,223 REFERENCE-COCKET WINDER: 15726A-000700 TELEPHONE: (415) 326-2400 |
|--|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|--|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

single TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-333-565-10 TYPE: amino acid STRANDEDNESS: sir

Query Match 100.0%; Score 84; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 5.4e-08; Matches 16; Conservative 0; Mismatches 0; Indels 1 ORYGRELRRMSDEFEG 16 δĀ

a

; 0

Gaps ; 0

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O
  Score 84; DB 1; Length 204;
Pred. No. 5.5e-07;
Mismatches 0; Indels
  Sequence 2, Application US/08661479

Patent No. 5834209

GENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Pall Alto
STAME: California
   /note= "Deduced amino acid sequence of mouse BAD."
   MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERALING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-UNN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
SOFTWARE: Patentin Release #1.0, Version #1.25
                                  CORGAIN TEPLLALALIN DAILS

APPLICATION UNDERS: US/08/33,565
FILING DATE: 31-OCT-1994
CLASSTFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
  NAME: Smith, William M
REGISTRATION UNDRES: 30,223
REPERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
  APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
   0
  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0;
   145 QRYGRELRRMSDEFEG 160
  1 QRYGRELRRMSDEFEG 16
  TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                      CURRENT APPLICATION DATA:
   TOPOLOGY: linear
MOLECULE TYPE: protein
   ZIP: 94301
COMPUTER READABLE FORM:
   ; NAME/KEY: Protein
; LOCATION: 1.204
; OTHER INFORMATION: /
US-08-333-565-2
  CITY: Pal
STATE: Ce
COUNTRY:
   RESULT 4
US-08-661-479-2
   ੍ਹ
ਰੂਹ
  δŽ
   ö
   0;
   100.0%; Score 84; DB 2; Length 23; ilarity 100.0%; Pred. No. 5.4e-08; Conservative 0; Mismatches 0; Indels
         US-08-661-479-10

Sequence 10, Application US/08661479

Sequence 10, Application US/08661479

Patent No. 5834209

Patent No. 5834209

TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

TITLE OF INVENTION: REGULATOR

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CUTY: Palo Alto

STATE: California

COUNTRY: US

COUNTRY: US
   US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622862
BENERAL INFORMATION:
APPLICANT: KORSMETER, Stanley J.
ITILE OF INVENTION: Bcl.x/Bcl.2 ASSOCIATED CELL DEATH
ITILE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
   ^{12}\mathrm{E} . Townsend and Townsend Khourie and Crew ^{379} Lytton Avenue
  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DAMA:

REPLICATION NUMBER: US/08/661,479
FILING DATE: 11-70N-1995
FILING DATE: 11-70N-1995
FILING DATE: 31-70N-1994
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M. REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
  ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  8 QRYGRELRRASDEFEG 23
   1 QRYGRELRRMSDEFEG 16
   LENGTH: 23 amino acids TYPE: amino acid
   STRANDEDNESS: single TOPOLOGY: linear
  ; MOLECULE TYPE: peptide US-08-661-479-10
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
   Query Match
Best Local Similarity
Matches 16; Conserv
   94301
  ADDRESSEE:
  SOFTWARE:
   RESULT 3
   셤
```

Gaps

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Sequence 13, Application US/08733505A
Sequence 13, Application US/08733505A
Sequence 13, Application US/08733505A
Sequence 13, Application US/08733505A
Set of the control 
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMETER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-7X/PGCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION: 60
   ö
  Length 204;
   Indels
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A FILING DATE:
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
   100.0%; Score 84; DB 2; 100.0%; Pred. No. 5.5e-07;
   Mismatches
   ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPAX: (314) 727-5092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
   ö
   145 QRYGRELRRMSDEFEG 160
   1 QRYGRELRRMSDEFEG 16
  CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
   : 204 amino acids amino acids
   Local Similarity 100.
Res 16; Conservative
  , MOLECULE TYPE: peptide US-08-733-505A-12
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   STREET: 7733 FORE CITY: ST. LOUIS STATE: MISSOURI COUNTRY: USA
   linear
  MISSOURI
  STRANDEDNESS
  FILING DATE:
  63105
  63105
   CITY: ST.
STATE: MJ
COUNTRY:
   LENGIH:
  Query Match
   ZIP:
   Matches
  RESULT 7
   à
  g
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0
   Gaps
  Gaps
  APPLICANT: KOREMEYER, STANLEY J.
APPLICANT: KOREMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
  0;
  .
0
  100.0%; Score 84; DB 2; Length 204; 100.0%; Pred. No. 5.5e-07;
  Length 204;
   /note= "Deduced amino acid sequence of mouse BAD."
  0; Indels
  0; Indels
  COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datem: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
  Score 84; DB 2; Pred. No. 5.5e-07;
   Mismatches
  Mismatches
  US-08-733-505A-12; Sequence 12, Application US/08733505A
   965458
   Sequence 1, Application US/08733505A Patent No. 5856445 GENERAL INFORMATION:
  FILING DATE:
CLASSIFICATION: 530
ATTORNETS:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
  ö
   ö
   145 QRYGRELRRMSDEFEG 160
   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
   1 QRYGRELRRMSDEFEG 16
   1 ORYGRELRRMSDEFEG 16
  Ouery Match
Best Local Similarity 100.(
Matches 16; Conservative
   TOPOLOGY: Linear
MOLECULE TYPE: protein
  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
   FEATURE:

NAME/KEY: Protein

LOCATION: 1..204

OTHER INFORMATION:

US-08-661-479-2
                          amino acid
   STREET: 7733 FOR CITY: ST. LOUIS STATE: MISSOURI
  COUNTRY: USA
ZIP: 63105
  STRANDEDNESS:
   US-08-733-505A-1
  US-08-733-505A-1
   RESULT 6
  RESULT 5
  g
   δ
   ŏ
  ДQ
```

Gaps

HOLLAND, DONALD R.

```
Sequence 3, Application US/09375257
Patent No. 6504022
GENERAL INFORMATION:
APPLICANT: HORNEW, William A.
TITLE OF INVENTION: HOWAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42801
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTERQ for Windows Version 4.0
  .
0
  ó
   GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE ON INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEGURNCES: 15
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
   Query Match 96.4%; Score 81; DB 4; Length 204; Best Local Similarity 93.8%; Pred. No. 1.8e-06; Matches 15; Conservative 1; Mismatches 0; Indels
   Length 204;
  96.4%; Score 81; DB 2; Length 204
93.8%; Pred. No. 1.8e-06;
tive 1; Mismatches 0; Indels
  APLANCE.
STREET: 4370 La JOLLA.
CITY: San Diego
STRATE: California
COUNTRY: United States
21P: 9212
COMPUTER READABLE FORM:
MEDIUM TYPE: PROPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SSP-1996
TARSTRICATION: 435
  ATTORNEY AGENT INFORMATION;
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEBRONE: (619) 535-9001
TELERAX: (619) 535-8949;
INFORMATION FOR SEQ ID NO: 3:
     RESULT 9
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
  145 QRYGRELRRWTDEFEG 160
   1 ORYGRELRRMSDEFEG 16
   SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
  Query Match
Best Local Similarity 93.8
Matches 15; Conservative
  ORGANISM: Mus musculus
US-09-375-257-3
  TYPE: amino acid
   TOPOLOGY: linear
  RESULT 10
US-09-375-257-3
   LENGTH: 204
  US-08-717-123-3
  SEQ ID NO 3
  TYPE: PRT
   Вb
   ö
   ó
   Gaps
  Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KARSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL.YL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
   .
0
   ó
  Query Match 100.0%; Score 84; DB 2; Length 204; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 16; Conservative 0; Mismatches 0; Indels
  100.0%; Score 84; DB 2; Length 204; 100.0%; Pred. No. 5.5e-07;
  0; Indels
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,505A
  0; Mismatches
  NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREST: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
REGISTRATION NUMBER: 35,197
REGISTRATION NUMBER: 965458
TELEPONE: (314) 727-5188
TELEPHONE: (314) 727-508
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   FILING NOMBER: 03/06/1330
FILING DATE: 03/06/1330
ATTORNET/AGENT INFORMATION: 03/06/1330
ATTORNET/AGENT INFORMATION: REGISTRATION NUMBER: 35/19/1
REPERBNCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
TELEPAX: (314) 727-5188
TELEFAX: (314) 727-5188
TELEPAX: (314) 727-5188
TELEPAX: (314) 727-5188
TELEPAX: (314) 727-5188
  1 QRYGRELRRMSDEFEG 16
   1 QRYGRELRRMSDEFEG 16
  : 204 amino acids
amino acid
  LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
  16; Conservative
  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14
  TOPOLOGY: linear
MOLECULE TYPE: peptide
  ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
   Query Match
Best Local Similarity
  US-08-733-505A-14
   US-08-733-505A-13
  COUNTRY:
   LENGIH:
  Matches
  qq
  g
   ğ
```

0

Gaps

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US-08-733-505A-57

Sequence 57, Application US/08733505A

Sequence 57, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION:

TITLE OF INVENTION:

SCHALES OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI
   Length 59;
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIble
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFRWARE: Patentin Release #1.0, Version #1.30
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
   Score 73; DB 2; L
Pred. No. 1.1e-05;
  Mismatches
   APPLICATION DATE:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
""" FPHONE: (314) 727-5188
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
  86.9%; Sura
100.0%; Pre
   REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPRONE: (314) 727-5188
TELEPRONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
   35,197
  FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLLAND, DONALD R.
REGISTRATION NUMBER: 35,19
  1 QRYGRELRRMSDEF 14
   46 ORYGRELRRMSDEF 59
  LENGTH: 59 amino acids
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  59 amino acids
   Query Match 86.9
Best Local Similarity 100.
Matches 14; Conservative
   ; MOLECULE TYPE: peptide US-08-733-505A-57
  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-733-505A-56
  TYPE: amino acid
STRANDEDNESS:
  linear
  amino acid
   COUNTRY: USA
ZIP: 63105
   STRANDEDNESS
  TOPOLOGY:
  δã
   q
   ö
   ; Sequence 56, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; TILLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL.XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; TITLE OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
; STATE: MISSOUR!
; COUNTRY USA
; ZIP: 63105
; COMPUTER READABLE FORM:
   Gaps
   APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL.XL/BCL.2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
   86.9%; Score 73; DB 2; Length 59; 100.0%; Pred. No. 1.1e-05; tive 0; Mismatches 0; Indels
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
OUMPUTER: INW PC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILL RELEASE #1.0, Version #1.30
CURRENT APPLICATION NAMBER: US/08/733,505A
  US-08-733-505A-55
; Sequence 55, Application US/08733505A
; Patent No. 5856445
   1 QRYGRELRRMSDEFEG 16
  1 ORYGRELRRMSDEF 14
   Best Local Similarity 100.
Matches 14; Conservative
   MOLECULE TYPE: peptide
   linear
   GENERAL INFORMATION:
APPLICANT: KORSMEY
  COUNTRY: USA
ZIP: 63105
  US-08-733-505A-55
   US-08-733-505A-56
  Query Match
  ŏ
                        ã
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Gaps .; 0

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Query Match 86.9%; Score 73; DB 1; Length 166; Best Local Similarity 100.0%; Pred. No. 3.4e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
  Search completed: September 15, 2003, 17:45:06 Job time : 9.34286 secs
  ATTORNEYAGENT 1890
ATTORNEYAGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31.794
REFERENCE/DOCKET NUMBER: CL-8
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
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   1 ORYGRELRRMSDEF 14
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TOPOLOGY: linear
  , MOLECULE TYPE: protein US-08-665-617-2
   TYPE: amino acid
                      32606
COUNTRY:
  LENGIH:
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  GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE, ADDRESS:
ADDRESSEB: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
INSOURI COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOUPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATCHILD Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/733,505A
  Gaps
   Gaps
  APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
   0
  0;
   86.9%; Score 73; DB 2; Length 59; 100.0%; Pred. No. 1.1e-05; Live 0; Mismatches 0; Indels
                    86.9%; Score 73; DB 2; Length 59; 100.0%; Pred. No. 1.1e-05; vative 0; Mismatches 0; Indels
  REPERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INPORMATION FOR SEQ. ID NO: 58:
SEQUENCE CHARACTERISICS:
LENGTH: 59 aming acids
  Sequence 58, Application US/08733505A Patent No. 5856445
  RESULT 15
US-08-665-617-2
Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
  FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
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  1 ORYGRELRRMSDEF 14
   46 QRYGRELRRMSDEF 59
   1 QRYGRELRRMSDEF 14
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Best Local Similarity 100.
Matches 14; Conservative
  14; Conservative
   TOPOLOGY: linear MOLECULE TYPE: peptide
  amino acid
                         Query Match
Best Local Similarity
  Florida
  .US-08-733-505A-58
   RESULT 14
US-08-733-505A-58
  CITY: (STATE:
   Matches
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0;

0; Gaps

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September 15, 2003, 17:25:56 ; Search time 12.6857 Seconds
(without alignments)
184.034 Million cell updates/sec
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   541936
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
  541936 segs, 145912426 residues
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
  1 QRYGRELRRMSDEFEG 16
   Minimum DB seq length: 0 Maximum DB seq length: 2000000000
   US-09-544-664-28
84
   Title:
Perfect score:
   Scoring table:
  Database :
  Sequence:
  Searched:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 258, Appl<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 147, Appl<br>Sequence 147, Appl<br>Sequence 18, Appl<br>Sequence 18, Appl<br>Sequence 18, Appl<br>Sequence 12, Appl<br>Sequence 12, Appl<br>Sequence 13, Appl<br>Sequence 14, Appl<br>Sequence 11, Appl<br>Sequence 11, Appl |
|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SUMMARIES<br>ID               | US-09-922-378-3<br>US-10-066-179-3<br>US-10-099-261-258<br>US-09-92-378-2<br>US-09-92-378-2<br>US-09-84-657-7<br>US-10-174-103A-147<br>US-10-174-103A-147<br>US-09-843-846-18<br>US-09-843-846-18<br>US-09-843-846-18<br>US-09-843-846-18<br>US-09-843-846-18<br>US-09-841-846-18<br>US-10-166-761-13594<br>US-10-166-087-16<br>US-10-166-087-16                     |
| DB                            | 4 50 4 50 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                              |
| %<br>Query<br>Match Length DB | 2044<br>2044<br>2046<br>2046<br>2046<br>2046<br>2046<br>2046                                                                                                                                                                                                                                                                                                         |
| %<br>Query<br>Match           | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                |
| Score                         | 88 1 2 2 2 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                         |
| Result<br>No.                 | 1111111<br>110000000000000000000000000000                                                                                                                                                                                                                                                                                                                            |

| Sequence 64, Appl | 62,              | Sequence 241, App | Sequence 570, App | Sequence 122, App | Sequence 11813, A   | Sequence 583, App | Sequence 97, Appl | H                   | 9                | П                 | 4                  | w                | Sequence 8, Appli | Sequence 8, Appli | 'n                 | Sequence 4, Appli | Sequence 10045, A   | Sequence 4658, Ap  | Sequence 36, Appl | Sequence 2, Appli | Sequence 10, Appl | Seguence 12463, A   | Sequence 4, Appli | Seguence 1577, Ap | Seguence 1237, Ap | Seguence 5539, Ap  | Sequence 1433, Ap  | 1788,     | Sequence 1789, Ap  |
|-------------------|------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|---------------------|------------------|-------------------|--------------------|------------------|-------------------|-------------------|--------------------|-------------------|---------------------|--------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-----------|--------------------|
| -09-971           | US-09-971-980-62 | US-10-092-750-241 | -10-10            | -10 - 14          | US-09-815-242-11813 | US-09-841-132-583 | US-10-007-693-97  | US-10-156-761-10435 | US-10-198-070-69 | US-10-121-757B-12 | US-09-738-626-4812 | US-09-794-715A-8 | US-10-286-581-8   | US-10-046-924-8   | US-09-815-242-5704 | US-10-047-412A-4  | US-10-156-761-10045 | US-10-106-698-4658 | US-09-949-029-36  | US-09-839-136-2   | US-09-839-136-10  | US-09-815-242-12463 | US-09-992-481-4   | $\overline{}$     | -083-35           | US-10-106-698-5539 | US-09-925-301-1433 | -09-925-3 | US-09-925-300-1789 |
| 10                | 10               | 15                | 15                | 15                | σ'n                 |                   | 4                 | 'n                  | ß                | iO                | 0                  | 0                | 13                | 'n                |                    | 寸                 |                     |                    |                   | 0                 |                   |                     |                   | 0                 | 15                | 15                 | σ                  | 10        | 10                 |
|                   | 64               | 138               | 327               | 385               | 571                 | 1053              | 1053              | 4840                | 1265             | 146               | 198                | 334              | 334               | 334               | 426                | 485               | 495                 | 515                | 556               | 575               | 575               | 705                 | 817               | 61                | 78                | 80                 | 87                 | 95        | 113                |
| 45.2              | 45.2             | 45.2              | 45.2              | 45.2              | 45.2                | •                 |                   |                     |                  | •                 | •                  | •                | •                 | -                 | 44.0               | •                 | 44.0                | 44.0               | 44.0              | 44.0              | •                 |                     |                   | 42.9              |                   |                    |                    | 42.9      | 42.9               |
| 38                | 38               | 38                | 38                | 38                | 38                  | 38                | 38                | 38                  | 37.5             | 37                | 37                 | 37               | 37                | 37                | 37                 | 37                | 37                  | 37                 | 37                | 37                | 37                | 37                  | 36.5              | 36                | 36                | 36                 | 36                 | 36        | 36                 |
| 16                | 17               | 18                | 19                | 20                | 21                  | 22                | 23                | 24                  | 25               | 26                | 27                 | 28               | 29                | 30                | 31                 | 32                | 33                  | 34                 | 35                | 36                | 37                | 38                  | 39                | 40                | 41                | 42                 | 43                 | 44        | 45                 |

## ALIGNMENTS

```
RESULT 1

US-09-922-370-3

Sequence 3, Application US/09922378

Sequence 3, Application US/09922378

Sequence 3, Application US/09922378

SEMERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Olteradorf, Tilliam A.

TITLE OF INVENTION: HOUSE AND METHODS OF USE

FILE REFERENCE: 4201-08-03

CURRENT RILKS DAFE: 2001-08-03

NUMBER OF SEO ID NOS: 15

SOFTWARE: FastSEO for Windows Version 4.0

SOFTWARE: FastSEO for Windows Version 4.0

SOFTWARE: PRT

ORGANISM: Mus musculus

GS-09-922-370-3

Ouery Match

Best Local Similarity 93.8%; Pred. No. 1.4e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps

Oy Inpergreneral Description US/10066179

Publication No. US20020115631A1

Sequence 3, Application US/10066179

Publication No. US20020115631A1

SEBSULT 2

US-10-066-179-3

SEQUENCE: ALINEMATION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE
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86.9%; Score 73; DB 9; Length 168; 100.0%; Pred. No. 0.00023; Live 0; Mismatches 0; Indels
  Score 73; DB 9; Length 168;
Pred. No. 0.00023;
  0; Indels
   COMPUTER: IDM COMPATIBLE
COMPUTER: IDM COMPATIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
FILING DATE: CURROWN-AMEN-3411199s, Lucy J.
NAME: BAILINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
   Snam, car.-
Corley, Neil C.
CITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
  Mismatches
   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
   APPLICANT: Hillman, Jennifer L.
   TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CERRACIPERSTICS:
LENGTH: 168 amino acids
  ; Sequence 1, Application US/09894657; Patent No. US20020098569A1; GENERAL INFORMATION:
  Query Match 86.9%; So
Best Local Similarity 100.0%; P.
Matches 14; Conservative 0;
   TYPE: amino acid
STRANDEDNESS: single
  STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM IYPE: DISKett
   LIBRARY: SYNORAB01
CLONE: 358673
  Yue, Henry
Lal, Preeti
Shah, Purvi
  1 QRYGRELRRMSDEF 14
   1 QRYGRELRRMSDEF 14
   TOPOLOGY: linear
  Best Local Similarity 100.
Matches 14; Conservative
  CITY: Palo Alto
  ; ORGANISM: Homo sapiens US-09-922-378-2
   IMMEDIATE SOURCE:
  US-09-894-657-1
   RESULT 6
US-09-894-657-7
   RESULT 5
US-09-894-657-1
  Query Match
  QQ
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  RESULT 3

US-10-059-261-258

US-10-059-261-258

Sequence 258, Application US/10059261

Publication No. US20030077826A1

SEMERAL INFORMATION:
APPLICANT: DACOTOT, ETIENNE DANIEL FRANCOIS

APPLICANT: BIEDMAN, JENA
TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE PROPERCY
TITLE OF INVENTION: PURCHICANT (PIPE)
TITLE OF INVENTION: PURCHICANT (PIPE)

TITLE OF INVENTION: PUPCHICANT (PIPE)

FILE REPERENCE: 03495.0216
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   ; OTHER INFORMATION: Description of Unknown Organism: TOX peptide US-10-059-261-258
  Query Match 96.4%; Score 81; DB 14; Length 204; Best Local Similarity 93.8%; Pred. No. 1.4e-05; Matches 15; Conservative 1; Mismatches 0; Indels
  S, ENCODING NUCLEIC USE
  Length 25;
   Indels
   Query Match

86.9%; Score 73; DB 15; L

Best Local Similarity 100.0%; Pred. No. 3.1e-05;

Matches 14; Conservative 0; Mismatches 0;
   Sequence 2.3 Application US/09922378
Fatent No. US20020037869al
GENERAL INFORMATION:
APPLICANT: HORDE, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, EW
FILE REFERENCE: 480140.42B3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILIAG DATE: 2001-08-03
CURRENT FILIAGE DATE: 2001-08-03
SOFTWARE: FRASESQ for Windows Version 4.0
                CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 204
  CURRENT APPLICATION NUMBER: US/10/059,261
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/265,594
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 325
   145 ORYGRELRRMIDEFEG 160
   1 QRYGRELRRMSDEFEG 16
  6 QRYGRELRRMSDEF 19
   1 QRYGRELRRMSDEF 14
FILE REFERENCE: 480140.428C1
   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 258
LENGTH: 25
   TYPE: PRT
ORGANISM: Unknown Organism
  ORGANISM: Mus musculus
   RESULT 4
US-09-922-378-2
  SEQ ID NO 2
LENGTH: 168
  US-10-066-179-3
   TYPE: PRT
   TYPE: PRT
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Gaps

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Gaps

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APPLICATION: TOTALING MOTIF-SPECIF
TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIF
TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHIN
FILE REPERENCE: CST-138 CIP3
CURRENT APPLICATION UNMER: US/10/174,105A
CURRENT PLING DATE: 100-04
PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR APPLICATION NUMBER: US 09/535,364
PRIOR FILING DATE: 1098-09-04
NUMBER OF SEQ ID NOS: 193 -
SOFTWARE: PATENTIAL OF SEQ ID NOS: 193 -
SOFTWARE: PATENTIAL OF SEQ ID NOS: 193 -
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SOFTWARE: PATENTIAL OF SEQ ID NOS: 193 -
SOFTWARE: PATENTIAL OF SEQ ID NOS: 193 -
SOFTWARE: PATENTIAL OF SEQ ID NOS: 193 -
SEQ ID NO 147
  NAME/KEY: MOD_RES

LOCATION: (8) ...(8)

CTERRION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-1058-147
  ;;
0
   ö
  86.9%; Score 73; DB 14; Length 168; 100.0%; Pred. No. 0.00023; Live 0; Mismatches 0; Indels
   79.8%; Score 67; DB 15; Length 15; 100.0%; Pred. No. 0.00017; Live 0; Mismatches 0; Indels
   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HAROO
APPLICANT: IKEDA, HAROO
APPLICANT: SHIRKAMA, HIROSHI
APPLICANT: SHIRK, TADAVOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATOORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILLE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
   APPLICANT: Cell Signaling Technology, Inc. APPLICANT: ZHANG, Hui APPLICANT: COMB, Michael J. APPLICANT: TAN, Xi
   Sequence 9145, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
  Sequence 147, Application US/10174105A Publication No. US20030068652A1 GENERAL INFORMATION:
  OTHER INFORMATION: Synthetic Peptide
  ORGANISM: Artificial Sequence
   1 ORYGRELRRMSDEF 14
  4 GRELRRMSDEFEG 16
  Query Match 86.9°
Best Local Similarity 100°
Matches 14; Conservative
   Best Local Similarity 100. Matches 13; Conservative
     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-179-2
   RESULT 8
US-10-174-105A-147
   US-10-156-761-9145
   Query Match
  TYPE: PRT
  FEATURE
   FEATURE:
   RESULT 9
  δŏ
   g
   g
   δ
  ;
0
  Gaps
   0;
   Sequence 2, Application US/10066179
Publication No. US20020115631A1
GENERAL INFORMATION:
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HORN BAD POLYBEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HORN BAD POLYBEPTIDES, COUSE
FILE REFERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT APPLICATION NUMBER: 202-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
  Query Match 86.9%; Score 73; DB 9; Length 168; Best Local Similarity 100.0%; Pred. No. 0.00023; Matches 14; Conservative 0; Mismatches 0; Indels
  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION NUMBER: 09/410,372
APPLICATION NUMBER: 09/410,372
APPLICATION NUMBER: 09/410,372
Sequence 7, Application US/09894657
Patent No. US20020098569Al
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Yue, Henry
Lal, Preeti
Shah, Purvi
Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
PROLIFERATION
   CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
   REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 550-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
  SEQUENCE DESCRIPTION: SEQ ID NO: 7:
   ATTORREY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
  LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
   108 QRYGRELRRMSDEF 121
  COMPUTER READABLE FORM:
   1 ORYGRELRRMSDEF 14
   LIBRARY: GenBank
CLONE: 1683637
   NUMBER OF SEQUENCES:
  COUNTRY: USA
ZIP: 94304
   IMMEDIATE SOURCE:
  STATE: CA
   US-10-066-179-2
   US-09-894-657-7
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Gaps

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0
   Length 582;
  Length 380;
   Query Match
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels
  47.6%; Score 40; DB 15; Length 38
63.6%; Pred. No. 1.2e+02;
Live 3; Mismatches 1; Indels
                           Indels
                             4;
  CHARLANT INVOLATION W.
APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Renneth C.
APPLICANT: Green, Jodie L.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
FILE REFERENCE: CULLANZ: Oldbac
CURRENT APPLICATION NUMBER: US/09/331,631A
CURRENT APPLICATION NUMBER: PCT/AU97/00874
PRIOR FILING DATE: 1997-12-22
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FEALSEQ for Windows Version 3.0
SEQ ID NO 22
SEQ ID NO 22
  Sequence 13594, Application US/10156761

Sublication No. US20030119018A1

GENERAL INNORMATION:
APPLICANT: OMORA. SATOSHI

APPLICANT: ISEHKAWA, JUN

APPLICANT: ISEHKAWA, JUN

APPLICANT: SATAN, HARUO

APPLICANT: SATAN, TOSHIUKI

APPLICANT: SATAN, TOSHIUKI

APPLICANT: SATAN, TOSHIUKI

APPLICANT: SATAN, USCHIUKI

APPLICANT: SAKAKI, YOSHIUKI

PRILE REFERENCE: 249-26

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 7001-06-07
  Best Local Similarity 43.8%; Pred. No. 21;
Matches 7; Conservative 5; Mismatches
   US-09-331-631A-22
, Sequence 2. Application US/09331631A
: Patent No. US20020168392A1
: GENERAL INFORMATION:
   Streptomyces avermitilis
  :|:||| | :| ||
533 ERHGREEREKEEEREG 548
   1 ORYGRELRRMSDEFEG 16
   1 ORYGRELRRMSDEFEG 16
   : |: | || |: :: || |: 22 RRFGEELERLLKKYEG 37
  PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13594
LENGTH: 380
  Query Match
Best Local Similarity 63.6
Matches 7; Conservative
  TYPE: PRT
ORGANISM: Maize
  RESULT 12
US-10-156-761-13594
   ) ORGANISM: Strep
US-10-156-761-13594
   US-09-331-631A-22
  δλ
   g
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  QΩ
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0
   Gaps
  .;
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  P.L.L.C
  SOFTWARE STAINS TO SOFTWARE STAINS STAINS TO SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,846
FILING DATE: 30-Apr-2001
CLASSIPICATION -CURNOWN>
PRIOR APPLICATION NUMBER: US 09/21,844
APPLICATION NUMBER: US 08/718,738
FILING DATE: 12-DEC-1998
APPLICATION NUMBER: US 08/463,382
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/460,104
FILING DATE: 02-UN-1995
APPLICATION NUMBER: PT/UN-1995
ATTORNEY/AGBRI INFORMATION:
   Query Match 59.5%; Score 50; DB 15; Length 215; Best Local Similarity 56.2%; Pred. No. 1.6; Matches 9; Conservative 4; Mismatches 3; Indels
  DB 9; Length 213;
   NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 1488.0730005/EKS/PSC
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
   CORRESPONDENCE ADDRESS:
RADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
   COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   ) MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-843-846-18
  51.2%; Score 43;
   STRANDEDNESS: not relevant
   Sequence 18, Application US/09843846 Patent No. US20020042362A1 GENERAL INFORMATION:
  ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-9145
  LENGTH: 213 amino acids TYPE: amino acid
   APPLICANT: KUNSCH, CHARLES A CHOPRA, ARVIND
   1 ORYGRELRRMSDEFEG 16
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9145
  TOPOLOGY: linear
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US-09-843-846-18
  Query Match
  LENGTH:
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Search completed: September 15, 2003, 17:47:52 Job time : 12.6857 secs
   5 RELRRMSDEF 14
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19 QELRRIGDEF 28
   , ORGANISM: Homo sapiens
US-10-092-750-1
          GENERAL INFORMATION:
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US-10-166-087-16
Squence 16, Application US/10166087
Squence 16, Application US/10166087
Squence 16, Application No. US20030077767A1
GENERAL INFORMATION:
APPLICANT: Branct, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
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; ORGANISM: Streptomyces refuineus subspecies thermotolerans
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Sequence 41, Application US/10146473
Publication No. US20030108888A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
  Sequence 1, Application US/10092750 Publication No. US20030032157A1
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  241 YEKELRRLADE 251
3 YGRELRRMSDE 13
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ORGANISM: Homo sapiens
   US-10-146-473-41
  RESULT 15
US-10-092-750-1
   Query Match
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   27
  Db
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  Gaps
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0
   Score 38; DB 15; Length 35;
Pred. No. 21;
2; Mismatches 1; Indels
APPLICANT: Halpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
APPLICANT: Alpin, Julia
TILEO FOR MAIGHT, MAILIN C.
TILE OF INVENTION: POLYPEPTIGES Interactive with BCL-X1
FILE REFERENCE: 50036/05002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT PILING DATE: 2002-03-07
PRIOR REPLICATION NUMBER: US 60/274,526
PRIOR PILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
EBNGTH: 35
   45.2%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Page

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2003, 17:18:16 ; Search time 7.2 Seconds
(without alignments)
213.708 Million cell updates/sec Run on:

1 ORYGRELRRMSDEFEG 16 US-09-544-664-28 84 score: Sequence: Title: Perfect :

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description           | bad protein - mous | r s    | probable two-compo | excinuclease ABC c | 2-dehydro-3-deoxy- | probable Fe-S oxid | hypothetical prote | 0      | gas-vesicle operon | oxidoreductase, so | phosphate ABC tran | phosphate ABC tran | regulatory protein | ATP-dependent 265 | vicilin-like stora | Antho-RFamide neur | Antho-RFamide prec | transforming prote | hypothetical prote | ~   | transcription requ | probable ATP-depen | óxoglutarate dehyd | desmoplakin I - ĥu | hypothetical prote | mevalonate kinase | NADH dehydrogenase | NADH dehydrogenase | NADH2 dehydrogenas |
|-----------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
|                       | !<br>!<br>!        |        |                    |                    |                    |                    |                    |        |                    |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |     |                    |                    |                    |                    |                    |                   |                    |                    |                    |
|                       | 1                  |        |                    |                    |                    |                    |                    |        |                    |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |     |                    |                    |                    |                    |                    |                   |                    |                    |                    |
| £                     |                    | H75403 | 303                | T36031             | S38185             | 7.1                | F84388             | JQ1128 | T08234             | F72289             | AB1762             | AH1386             | RGBYC3             | G69496            | B53234             | A39172             | A44308             | 636                | ***                | 133 | 54                 | 388                | 997                |                    | 569                | 99                | 9102               | H85868             | Ō                  |
| DB                    | ~                  | 7      | 7                  | 7                  | 7                  | 7                  | 7                  | ~      | C)                 | 7                  | 7                  | 7                  | Н                  | 7                 | 7                  | 7                  | 7                  | 7                  | C                  | 7   | ~                  | ~                  | ~                  | ~                  | ~                  | 7                 | ~                  | 7                  | ~                  |
| Length                | 204                | 564    | 463                | 1014               | 370                | 445                | 84                 | 113    | 113                | 220                | 271                | 271                | 322                | 398               | 583                | 334                | 435                | 206                | 219                | 374 | 411                | 887                | 296                | 2677               | 5138               | 310               | 910                | 910                | 910                |
| %<br>Query<br>Match 1 | 100.0              | 52.4   |                    | 0                  | 50.0               | 50.0               | ω.                 |        |                    |                    | •                  | 48.8               | œ                  |                   | 8                  | •                  | 48.2               | ٠                  | •                  | ٠   | 47.6               | ٠                  | •                  |                    |                    |                   | 7.                 | •                  | 47.0               |
| Score                 | 84                 | 44     | 43                 | 42.5               | 42                 | 42                 | 41                 | 41     | 41                 | 41                 | 41                 | 41                 | 41                 | 41                | 47                 | 40.5               | 40.5               | 40                 | 40                 | 40  | 40                 | 40                 |                    | 40                 | 40                 | σ,                | 39.2               | o,                 | φ.                 |
| Result<br>No.         |                    | 2      | m                  | 4                  | ស                  | 9                  | 7                  | 80     | o                  | 10                 | 11                 | 12                 |                    | 14                |                    | 16                 | 17                 | 18                 | 19                 | 20  | 21                 | 22                 | 23                 | 24                 | 25                 | 26                | 27                 | 28                 | 29                 |

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Gaps 0;

Query Match 52.4%; Score 44; DB 2; Length 564; Best Local Similarity 61.5%; Pred. No. 23; Matches 8; Conservative 3; Mismatches 2; Indels

| NADH2 dehydrogenas | NADH2 dehydrogenas | hypothetical prote | hypothetical prote | ribosomal protein | hypothetical prote | floral homeotic pr | transporter homolo | hypothetical prote | DNA repair protein | RAD51 protein homo | hypothetical prote | probable inositol | inositol-1,4,5-tri | excinuclease ABC c | cobalamin biosynth |
|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| AI0796             | AD0311             | AC3365             | A82928             | T26996            | B84184             | A42095             | C69808             | T39444             | E90121             | S42107             | T32163             | H84727            | T48113             | H75356             | G83278             |
| N                  | 7                  | 7                  | 7                  | 7                 | 7                  | 7                  | N                  | N                  | 7                  | 7                  | 7                  | 7                 | 7                  | 7                  | 7                  |
| 910                | 914                | 73                 | 87                 | 16                | 105                | 232                | 275                | 315                | 331                | 365                | 380                | 501               | 574                | 1016               | 1248               |
| 47.0               | 47.0               | 46.4               | 46.4               | 46.4              | 46.4               | 46.4               | 46.4               | 46.4               | 46.4               | 46.4               | 46.4               | 46.4              | 46.4               | 46.4               | 46.4               |
| 39.5               | 39.5               | 39                 | 39                 | 39                | 39                 | 39                 | 39                 | 39                 | 39                 | 39                 | 39                 | 39                | 39                 | 39                 | 39                 |
| 0                  | _                  | C)                 | m                  |                   | 10                 |                    | _                  | 38                 | 39                 | 40                 |                    | ~1                | ~                  | 44                 | 10                 |

## ALIGNMENTS

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Data protein - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house) (Species: Os-Mar-1995 #sequence_xevision 03-Mar-1995 #sequence_xevision 03-Mar-1995 #sequence_xevision (Species: Data of Species: Os-Mar-1995 #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #sequence number: AS-5671; MulD:95136361; PMID:7834748 #sequence number: AS-5671 #sequence os-Mar-1995 #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #sequence (Species: Os-Mar-1995) #squence (Species: Os-Ma
  glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevam, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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R;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.
Yeast 9, 1131-1137, 1993
Y;Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A;Reference number: S38185; MUID:94078675; PMID:8256522
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R; Kuencler, M.; Paravicini, G.; Eqli, C.M.; Irniger, S.; Braus, G.H.
Gene 113, 67-74, 1992
   A;Title: Clouing, primary structure and regulation of the ARO4 gene, encoding the tyr A;Reference number: JN0322; MUID:92225349; PMID:1348717
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A;Renarler, M.; Balmelli, T.; Eggli, C.M.; Paravicini, G.; Braus, G.H.
A;Title: Clouing, primary structure, and regulation of the HIS7 gene encoding a bifun A;Reference number: A48651; MUID:93374850; PMID:8366040
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A, Molecule Lype: DNA
A, Residues: 352-370 (KU2>
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A, Gene: SGD:ARO4
A, Cross-references: SGD:S0000453; MIPS:YBR249c
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A.Description: aldehyde-lyase; carbon-carbon lyase
A.Description: aldehyde-lyase; carbon-carbon lyase
A.Pathway: aromatic amino acid biosynthesis; shikimate pathway
A.Note: first step in shikimate pathway
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  ore 42; DB 2; Length 370; ed. No. 32; Mismatches 5; Indele
  R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
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G97123
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   CyAccession: H83036
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Rickey, M.J.; Er adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAOL, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83036
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C;Genetics:
A;Gene: PA4886
C;Superfamily: hypothetical protein HII707; sensor histidine kinase homology
   S38185
2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cd
N.Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthase;
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   50.6%; Score 42.5; D
66.7%; Pred. No. 75;
tive 1; Mismatches
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   51.2%;
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Best Local Similarity
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  368
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   Matches
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us-09-544-664-28.rpr

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Matches 7; Conservative
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  A; Status: preliminary
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   C; Genetics:
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  RESULT 9
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R;Jones, J.G.: Young, D.C.: DasSarma, S.
Gnne 102, 117-122, 1991
Gnne 102, 117-122, 1991
A;Title: Structure and organization of the gas vesicle gene cluster on the Halobacterium A;Reference number: JQ1122; MUID:91323716; PMID:1864501
  in
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
  A;Note: the source is designated as Halobacterium halobium
R;Horne, M.; Englert, C.; Wimmer, C.; Pfeifer, F.
Mol. Microbiol. 5, 1159-1174, 1991
A;Title: A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis:
A;Reference number: 815183; MUID:92065812; PMID:1956294
   gas-vesicle operon protein gvpK - Halobacterium salinarum plasmids pHH1 and pNRC100
C;Species: Halobacterium salinarum
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-2000
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  ö
  A; Residues: 1-445 < KUR>
A; Cross-references: GB: ABC01437; PIDN: AAK79778.1; PID: 915024787; GSPDB: GN00168
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Best Local Similarity 46./*
7; Conservative
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A, Status: preliminary
A, Molecule type: DNA
   A; Accession: S15190
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Alvariety: strain NRC-1

C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000

C; Accession: T08234

C; Accession: T08234

R; Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, Senome Res. 8, 1131-1141, 1998

A; Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid A; Reference number: 216408; MJID:99063795; PMID:9847077
A, Molecule type: DNA
A, Residues: 1-13 <-HORN-
A, CROSs-references: EMBL:X55648; NID:g43516; PID:g43524
A, Seperation tal source: plasmid pHH1
A, Genetics: PHH
A, Shore: the nucleotide sequence was submitted to the EMBL Data Library, September 19:
A, Note: the source is designated as Halobacterium halobium
C, Genetics: <NRC>
  Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72289
  A;Cross-references: GB:AE001772; GB:AE000512; NID:94981693; PIDN:AAD36230.1; PID:949
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   C.Species: Thermotoga maritima
C.Date: 11-0nu-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C.Accession: F72289
R.Nelson, K.E.: Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haff, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
   gas-vesicle operon protein gvpK - Halobacterium sp. (strain NRC-1) plasmid pNRC100 N;Alternate names: hypothetical protein H0228 C;Species: Halobacterium sp.
   ö
  ó
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A):Cross-references: EMBL:AF016485, NID:92822278, PID:92822295, HALOSP:H0228
A):Experimental source: strain NRC-1
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N.Alternate names: CAT3 protein; protein G2945; protein VGL115w
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C.Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jul-2000
C.Accession: A38906; JT0316; S48508; S64125
R.Ycelenza, J.L.; Engy F.J.; Carlsou, M.
Mol. Cell. Biol. 9, 5445-5054, 1989
A.Title: Molecular analysis of the SNR4 gene of Saccharomyces cerevisiae: evidence for A;Reference number: A33480; MUTD: 90097921; PMID: 2481228
A.Accession: A38906
A.Molecule type: DNA
A.Residues: 1-322 CB:M30470; NID: 9172635; PIDN: AAA35061.1; PID: 9172636
R.Schueller, H.J.; Entian, K.D.
Gene f), 247-257, 1988
A.Reference number: JT0316; MUID: 89006284; PMID: 3049255
A.Accession: JT0316
A.Reference number: JT0316; MUID: 89006284; PMID: 3049255
A.Residues: 1-322 CSCH>
A.Reference number: JT0316; MUID: 89006284; PMID: 3049255
A.Residues: JT0316
A.Reference number: S48807
A.Reference number: S48807
A.Reference number: S48807
A.Reference number: ARBOR
  C, Accession: G69496
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Doč., Fleischmann, B.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, F. Glodek, A.; Zhou, L.; Oyerbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
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A; Residules: 1-21 <DOI>
A; CERSIDULES: 1-21 <DOI>
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R; Lauquin, G.
Submitried to the Protein Sequence Database, May 1996
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G;Fubction:
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YLRALNRMNDEIDG 79
                            YGRELRRMSDEFEG 16
  4 GRELRRMSDEFEG 16
   8; Conservative
  Best Local Similarity
Matches 8; Conserv
                            m
   99
  Query Match
  RESULT 14
G69496
   RESULT 13
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   g
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   phosphate ABC transporter (ATP-binding protein) homolog lin2639 [imported] - Listeria in C; Species: Listeria innocua C; Species: Listeria innocua C; Species: Listeria innocua C; Species: Listeria innocua C; Date: 27.Nov-2001 #text_change 17-May-2002 C; Accession: AB1762 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker J. Dominguer-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kinno, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species
A; Reference number: AB1762 A; Status: preliminary A; Molecule type: DNA A; Mo
   A;Status: preliminary
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A;Residues: 1-271 GLA>
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   C;Genetics:
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  Best Loc
Matches
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   δğ
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A/Authors: Otterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A.Reference number: A69250; MuID:98049343; PMID:9389475
A.Recession: 669496
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
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A.Residues: 1.398 (KLE)
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F.155-365/Domain: FLSM/SEC18/CDC48 type ATP-binding domain homology <VARP>
F.182-189/Region: nucleotide-binding motif A (P-loop)
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Nyalternate names: globulin-1L
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C.Species: Zea mays (malze)
C.Species: Zea mays (malze)
C.Bacession: B53234; S21824
R.Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A.Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.
A.Reference number: A53234; MUID:92090707; PMID:1752424
A.Status: preliminary
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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|           | Description      | 061337    |         |           |            |           |         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |            | _          |            | caeno      |            |            | Q9hv01 pseudomonas | clost     | 043521 homo sapien |
|-----------|------------------|-----------|---------|-----------|------------|-----------|---------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|--------------------|-----------|--------------------|
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| ď         | Query<br>Match I | 100.0     | 00      | 86.9      | 50.6       | 50.0      | 50.0    | 50.0       | 50.0       | 48.8       | 48.8       | 48.8       | 48.8       | 48.8       | 48.2       | 48.2       | 48.2       | 47.6       | 47.6       | 47.6       | 47.0       | 47.0       | 46.4       | 46.4       | 46.4      | 46.4       | 46.4       |            |            |            |            | 45.8               |           |                    |
|           | Score            |           | 84      | 73        | 42.5       | 42        | 42      | 42         | 42         | 41         | 41         | 41         | 41         | 41         | 40.5       | 40.5       | 40.5       | 40         | 40         |            | 39.5       |            | 39         | 39         | 30        | 39         | 39         | 39         | 39         | 38         | 38.5       | 38.5               | 38        | 38                 |
|           | Result<br>No.    |           | CI      | m         | 4          | ĸ         | 9       | 7          | 80         | 6          | 10         | 11         | 12         | 13         | 14         | 15         | 16         | 17         | 18         | 19         | 20         | 21         | 22         | 23         | 24        | 25         | 26         | 27         | 28         | 29         | 30         | 31                 | 32        | 33                 |

| Q9uzq5 pyrococcus P79023 candida alb P83094 drosophila P2079 homo sapien P34160 saccharomyc Q9p193 chlamydia in Q84834 chlamydia it Q00341 homo sapien P81021 gallus gallu P81021 gallus gallu P81367 micrococcus Q9aqc8 buchnera ap |            | 204 AA.<br>update)<br>on update)<br>(Bc1-2 binding component<br>romoter).                                                                    | ertebrata; Buteleostomi;<br>i; Muridae; Murinae; Mus.                               | Thompson C.B., Korsmeyer S.J.;<br>, and Bcl-2, displaces Bax and                                                                    | 12 AND SER-136.<br>Herrera R., Nunez G.;<br>BAD through the protein                                                                                                                                 | Fesik S.W., Yaffe M.B.,<br>perate to inactivate BAD by       | sfully competes for the thereby affecting the level ns with BAX. Can reverse the but not that of Bol-2. th factor receptor signaling | c and the apoptotic pathways with the anti-apoptotic proteins, Bcl-x(1), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  x(1), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  CC x(1), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).  CC -1 SUBCELUIAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm.  CC -1 DOMAIN: Intact BH3 domain is required by BIK, BLD BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.  CC -1 PTM: Phosphorylated on Ser-112 in response to survival stimuli.  CC vir PTM: Prosphorylated on Ser-112 in response the percodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(1) and the promotion of cell survival.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 THIE_PYRAB 1 AROG_CANAL 1 STIM_DROME 1 PERL_HUMAN 1 CRR1_CHLMU 1 RIR1_CHLMU 1 VGLN_HUMAN 1 VGLN_HUMAN 1 VGLN_CHICK 1 UBR1_SCHPO 1 UVRA_MICLU 1 LEU3_BUCUL 1 LEU3_BUCUL                                                             | ALIGNMENTS | PRT;<br>ted)<br>sequence<br>annotatin<br>ath (BAD)                                                                                           | lata; Craniata; Vertebrata;<br>ntia; Sciurognathi; Muridae;                         | L.H.,<br>Bcl-XI                                                                                                                     | GENESIS OF SER-11<br>9381178;<br>ccia M., Page C.,<br>nosphorylation of                                                                                                                             | IDDUES.<br>=10949026;<br>1 L., Petros A., I                  | ell death. Successell death. Successell death. Successell. of these proteit ity of Bcl.*x(L).                                        | himass with the an also binds protection of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of                            |
| 45.2 207<br>45.2 370<br>45.2 370<br>45.2 570<br>45.2 1047<br>45.2 1047<br>45.2 1268<br>44.6 992.                                                                                                                                     |            | ANDA!<br>35,<br>35,<br>41,<br>f cel                                                                                                          | s (Mouse).<br>Metazoa; Chordata;<br>utheria; Rodentia;<br>10090;                    | OM N.A.<br>n, and Thymus;<br>36361; PubMed=783<br>ad J., Jockel J.,<br>erodimeric partne<br>11 death.";                             | PHOSPHORYLATION, AND MUTAGENESIS O<br>MEDLINE-98022383; Pubmed=9381178;<br>Del Peso L., Gonzalez-Garcia M., P.<br>"Interleukin-3-induced phosphoryla<br>kinase Akt.";<br>Czience 278:687-689(1997). | OF SERINE RESTANSORY PUDMED TRESORY A., H. Ratsov A., H. E.; | prospinory factors (141-51(2000). W: Promotes of to Bclx(L). prodimerization epressor active to act as a                             | a apoptotic par<br>1. Forms heters<br>1. 12. and Bc1-<br>1.12./ear-136<br>JUAR LOCATION<br>Intact BH3 do<br>Intact BH3 do<br>Intact physicate<br>their pro-apo<br>their pro-apo<br>their pro-apoptotic in<br>the physicated<br>their physicated<br>their and a service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in service in se |
| 3.44<br>3.35<br>3.35<br>3.35<br>3.38<br>3.38<br>3.38<br>3.38<br>3.44<br>3.7<br>3.7<br>3.7<br>3.7<br>3.7<br>3.7<br>3.7<br>3.7<br>3.7<br>3.7                                                                                           |            | SULT 1 D_MOUSE BAD_MOUSE ST; Q61337; 01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 28-FEB-2003 (Rel. EC12-antagonist o. 6) (Ec1-xL/Bc1-2. BAD OR BBC6. | Mus musculus (Mouse). Eukaryota; Metazoa; C Mammalia; Eutheria; R NCBI_TaxID=10090; | LISSUE-Brain, and I<br>TISSUE-Brain, and I<br>MEDLINE-55136561; Brang E., Jr. Jr. Trang E., Jr. Jr. Jr. Jr. Jr. Jr. Jr. Jr. Jr. Jr. | PHOSPHORYLA<br>MEDLINE=980<br>Del Peso L.<br>"Interleuki<br>Kinase Akt.<br>Science 278                                                                                                              | NUTAGENESIS MUTAGENESIS MEDLINE=204 Datta S.R., Greenberg M  | MOL. Cell 6 -!- binding of hete death r Appears                                                                                      | and the  "(L), B  "(L), B  "Is Ser  "Is                           |
|                                                                                                                                                                                                                                      |            |                                                                                                                                              |                                                                                     |                                                                                                                                     | RY<br>RY<br>RY<br>RI<br>RI                                                                                                                                                                          | R R R R R R R R R R R R R R R R R R R                        | Z                                                                                                                                    | 8888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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   ó
  S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION; INTERACTS WITH
  Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bcl.xL/Bcl.2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
  D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in
Ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
  Gaps
  PKB).
PKB).
PKB).
   ;
  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BC12-antagonist of cell death (BAD) (BC1-2 binding component
6) (BC1-xL/BC1-2 associated death promoter).
   Length 204;
  [1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
TISSUE-CVARY;
         major site of profein kinase A (CAPK) phosphorylation. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
  PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND PHOSPHORYLATION (BY PKA AND
   Indels
   6C2BA910205053F7 CRC64;
  100.0%; Score 84; DB 1; L
100.0%; Pred. No. 1.3e-06;
Live 0; Mismatches 0;
   SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
   205 AA.
  BCL-X(L)
   Neurosci. Lett. 243:137-140(1998).
   MEDLINE=21109372; PubMed=11161472;
   MEDLINE=98194755; PubMed=9535132;
  MGD; MGT:1096330; Bad.
InterPro; IPR000712; Bcl2_BH.
PROSITE; PR001259; BH3; FALSE_NBG.
Apoptosis; Phosphorylation.
  MEDLINE=98034386; PubMed=9369453;
   22080 MW;
  1 QRYGRELRRMSDEFEG 16
  EMBL; L37296; AAA64465.1; -.
  Conservative
   STANDARD;
  BAD_RAT STANDARD (035147; 070256; 09JHX1;
  (Rat)
  PIR; A55671; A55671.
   204 AA;
  Best Local Similarity
Matches 16; Conserv
  HSSP; Q92934; 1G5J
  SEQUENCE FROM N.A.
  Rattus norvegicus
  NCBI_TaxID=10116;
  brain."
  IISSUE-Brain
   TISSUE=Brain
   Query Match
  SEQUENCE
  MOD_RES
   MOD_RES
MUTAGEN
MUTAGEN
  the rat
   MUTAGEN
  DOMAIN
   RESULT 2
  BAD_RAT
  g
   QΣ
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                       their interaction with Bel-w in sympathetic neurons.";

their interaction with Bel-w in sympathetic neurons.";

Mol. Cell. Neurosci. 7:39-106(2001).

-!- FUNCTION: Promotes cell death. Successfully competes for the binding to Rel-Kil, Bel-s and Bel-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bel-Kil, but not that of Bel-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.

-!- SUBGNUT: Forms heterodimers with the anti-apoptotic proteins, Bel-Xil, Bel-2 and Bel-w. Also binds protein S100AlO. The Ser-113/Ser-137 phosphorylated form binds 14-3-3 proteins.

-!- SUBGELIULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, locates to the cytoplasm (By similarity).

-!- ATTERNATIVE PRODUCTS:
   S->A: NO HETERODIMERIZATION WITH 14-3-3
PROTEINS NO EFFECT ON HETERODIMERIZATION
WITH BECL3 NOR WITH PROTEIN P11.
7AGGR -> ERGRK (IN REF. 1).
7AGGR -> GRGRK (IN REF. 1).
  (BY SIMILARITY).
LPRPKSAGTATØMRQSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELIYSVEFLPVRAIAMEGWPLLWSPQSFPHTLPPTPP
  DOMAIN: Interest BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

PTM: Phosphorylated on Ser-131 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-156, a site within the BH3 domain, leading to the release of Bcl-XtL) and the promotion of cell survival. Ser-137 is the major site of AKKZPKB phosphorylation, Ser-156 the
  TISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more
   /FIId=VSP_000534.
S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D., "Functional characterization of two splice variants of rat BAD and
   EVAMFPLRYWTALRRLC (in isoform Beta)
  (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
   PHOSPHORYLATION (BY PKA AND PKB)
   (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
   major site of protein kinase A (CAPK) phosphorylation (By
   similarity).
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
   Phosphorylation; Alternative splicing.
  Event=Alternative splicing; Named isoforms=2;
  IsoId=035147-2; Sequence=VSP_000534;
   IsoId=035147-1; Sequence=Displayed;
   BH3
  ; IPR000712; BC12_BH. PS01259; BH3; FALSE_NEG.
   EMBL, AF003523; AAC53374.1; -. EMBL; AF031227; AAC15100.1; -. EMBL; AF279910; AAF91427.1; -.
   34 SI
22228 MW;
   EMBL; AF279911; AAF91428.1; -. HSSP; Q92934; 1G5J.
  113
   137
  156
   205
  113
  137
   29
205 AA;
   abundant form.
  156
   137
   166
  113
  137
  Name=Alpha;
  Name=Beta;
  InterPro; ]
PROSITE; PS
  Apoptosis;
   CONFLICT
   /ARSPLIC
   MOD_RES
   MOD_RES
  MOD_RES
  MUTAGEN
  MUTAGEN
```

Š g

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SEQUENCE
  Query Match
   MOD_RES
  MOD_RES
   VARIANT
   MOD_RES
   HELIX
TISSUE-LAUNG;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Alausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

XX Alackul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Roltschul S.F., Jordan H., Moore T., Max S.I., Wang J., Bisieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Stapeton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

XX Nilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.M., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Xzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Raching Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Ren Schein J. B., Jones S.J.M., Marra M.A.;

RR Generation and initial analysis of more than 15,000 full-length

Ruman and mouse cDNA sequences.";
  6
  SEQUENCE FROM N.A.
Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
"A human protein that interacts with Bcl-2 and have homology to mouse
   BAD_HUMAN STANDARD, PRT; 168 AA.
092934; 014803;
01-007-2001 (Rel. 35, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 43, Last annotation update)
17-SEP-2003 (Rel. 43, Last annotation update)
18-SEP-2003 (Rel. 43, Last annotatio
   Gaps
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  Wang Y., Wilson G.,
  0
               Score 84; DB 1; Length 205;
Pred. No. 1.3e-06;
; Mismatches 0; Indels
   MEDLINE-97083574; PubMed-8929532;
Wang H.-G., Rapp U.R., Reed J.C.;
"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
  Takayama S., Reed J.C.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
  Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
  SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
   Ottilie S., Diaz J.-L., Borne W., Chang J., War
Chang S., Weeks S., Fritz L.C., Oltersdorf T.,
"Dimerization properties of human BAD.";
J. Biol. Chem. 272:30866-30872(1997).
   SEQUENCE FROM N.A., AND DIMERIZATION.
   TISSUE=Bone marrow;
MEDLINE=98049554; PubMed=9388232;
  0;
  100.0%;
   1 QRYGRELRRMSDEFEG 16
           Query Match
Best Local Similarity 100.0
Watches 16; Conservative
   cell 87:629-638(1996)
  Homo sapiens (Human)
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCBI_TaxID=9606
  TISSUE=Lung;
  146
   BAD HUMAN
```

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  mutagenesis, and biophysical studies...
Protein Sci. 9:2528-2534(2000).

-!- FUNCITION: Promotes cell death. Successfully competes for the binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
-- SUBUNIT: Porms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By
   CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
   phosphorylation, locates to the cytoplasm.

-:- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-:- DOMAIN: Intact BH3 domain is required by BIK, BLD, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.
-:- PTM: Phosphorylated on Ser-75 in response to survival stimuli. Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-99 is the major site of AXI/FKB phosphorylation, Ser-118 the major site of protein kinase A (CAPK) phosphorylation (by
STRUCTURE BY NMR OF 103-127.

BEDDINE-21073551, PubMed-11206074;
PETDOS A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
   "Rationale for Bcl-xL/Bad peptide complex formation from structure,
  PHOSPHORYLATION (BY PKA AND PKB) (BY
  (BY
  SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
  PHOSPHORYLATION (BY PKA AND PKB)
  SIMILARY).
SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
  86.9%; Score 73; DB 1; Length 168;
  SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
  Apoptosis; Phosphorylation; Polymorphism; 3D-structure.
DOMAIN 110 124 BH3.
  SIMILARITY).
A -> S (in dbSNP:3729933).
   18392 MW; 69FD8D27DDEE3241 CRC64;
   GO; GO:0005741; C:mitochondrial outer membrane; NAS. GO: GO:0005515; F:protein binding activity; NAS. GO; GO:0006322; P:apoptotic program: TAS. InterPro; IPRO00712; Boltz_BH. PROSITE; PS01259; BH3; FALSE_NEG.
   FTIG=VAR_015380.
   SIMILARITY
   EMBL, U66879; AAB36516.1; ALT_FRAME.
EMBL, AF021792; AAB72092.1; -
EMBL, AF031523; AAB88124.1; -
EMBL, BC001901; AAH01901.1; -
  GO; GO:0005737; C:cytoplasm; NAS. GO; GO:0005741; C:mitochondrial or GO; GO:0005515; F:proresin binai-
   99
  118
   107
  Genew; HGNC:936; BAD.
   PDB; 1G5J; 07-FEB-01.
   168 AA;
   similarity).
   66
  118
   107
  similarity)
  Mack J., Swi
Fesik S.W.;
  603167
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VARSPLIC
  RESULT 5
   δŽ
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             0
   lesions (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
   "Complete genome sequence of the model actinomycete Streptomyces obelicotor A3(2)."

Nature 417.141-147(2022).

-I- FUNCTION: The UNTABC repair system catalyzes the recognition and processing of DNA lesions. UVTA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvra and 2 uvrB subunits scans DNA for abnormalities. When the presence of a
   PIR: 736031; 736031.

InterPro: IPR003439; ABC_transporter.

InterPro: IPR004602; UVIA.

Pfam: PP000005; ABC_trans; 2.

PGRTAMS; TIGR00630; UVIZ; 1.

PROSITE: PS00211; ABC_TRANSPORTER_1; 2.

PROSITE: PS50893; ABC_TRANSPORTER_1; 2.

SOS response: Excision nuclease; DNA recombination; DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
              Gaps
   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVTABC system protein A (UVTA protein) (Excinuclease ABC subunit A).
UVRA OR SC01958 OR SCC54.18C.
  STRAIN-A3(2) / M145;

MEDLINE-219964(10) PubMed=12000953;

MEDLINE-219964(10) PubMed=12000953;

Bentley S.D., Chater K.E., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Nell S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Ruther S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
   lesion has been verified by uvrB, the uvrA molecules dissociate
  (By similarity).
-:- SUBUNIT: Forms a heterotetramer with uvrB during the search for
             0;
   Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
   32 39 ATP (POTENTIAL).
645 652 ATP (POTENTIAL).
744 770 C4-TRY (C4-TRY OR4D6B18692A792D CRC64;
              Indels
Pred. No. 6.7e-05;
Mismatches 0;
   PRT; 1014 AA.
             ;
0
   Zinc-finger; Complete proteome
NP_BIND 32 39 AS
  EMBL; AL035591; CAB38148.1; -.
 100.08;
   108 ORYGRELRRMSDEF 121
  1 QRYGRELRRMSDEF 14
              14; Conservative
  STANDARD;
Best Local Similarity
  [1]
SEQUENCE FROM N.A.
   NCBI_TaxID=1902;
  Hopwood D.A.;
   UVRA_STRCO
   NP_BIND
ZN_FING
SEQUENCE
  RESULT 4
UVRA_STRCO
              Matches
  ð
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  Ä
   TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B-AND T-LYMPHOID CELL
  Gaps
  BAX OR BAK (BY SIMILARITY).
SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES.
ALTERNATIVE PRODUCTS:
  SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
  EMBO J. 17:384-395(1998).

-!- FUNCTION: INDUCES APOPTOSIS. THE ISOFORMS VARY IN CYTOTOXICITY
WITH ISOFORM BIMS BEING THE MOST POTENT AND ISOFORM BIMEL BEING
THE LEAST POTENT.
   Cory S., Huang D.C.S., "Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
   O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
   BIM_MOUSE STANDARD; PRT, 196 AA.
054919; 054910; 054910;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
BCL2-like protein 11 (BCL2 interacting mediator of cell death).
  ä
Length 1014;
   -!- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
  SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
  -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
  Indels
   Missing (in isoform BimL).
/FTId=VSP_000536.
Missing (in isoform BimS).
/FTId=VSP_000537.
   Event=Alternative splicing; Named isoforms=3;
DB 1;
                               Pred. No. 39;
1; Mismatches
   IsoId=054918-2; Sequence=VSP_000536;
  Apoptosis; Alternative splicing; Membrane.
DOMAIN 146 160 BH3.
VARSPLIC 42 97 Missing (in is
  IsoId=054918-3; Sequence=VSP_000537;
  IsoId=054918-1; Sequence=Displayed;
Score 42.5;
   SPECIFICITY, AND ALTERNATIVE SPLICING.
MEDLINE-98094360; PubMed-9430630;
  EMBL; AF032459; AAC40029.1; -.
EMBL; AF032460; AAC40030.1; -.
EMBL; AF032461; AAC40031.1; -.
MGD; MGI:1197519; Bc12111.
InterPro; IRR00712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
   368 RYGRE-RRYTTAFEG 381
  2 RYGRELRRMSDEFEG 16
Query Match
Best Local Similarity 66.7
Matches 10; Conservative
   127
  Mus musculus (Mouse).
  NCBI_TaxID=10090;
  CYTOTOXICITY.
   42
  Name=BimEL;
   Name=BimL;
  Name=BimS;
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104
104
146
   42
  STRAIN-S288c;
  STRAIN-S288c
   Kuenzler M.;
   AROG_YEAST
  Apoptosis;
   Submitted
  Query Match
Best Local S
   SEQUENCE
  INIT_MET
   VARSPLIC
   VARSPLIC
  CONFLICT
  CHAIN
  AROG_YEAST
   Matches
  RESULT
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   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ó
  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
   FUNCTION: INDUCES APOPTOSIE.
SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
BAX OR BAK.
SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES
   Comment=2 isoforms, BOD-L (shown here) and BOD-S, are produced by alternative initiation at Met-1 and Met-104; TISSUE SPECIFICITY: Widely expressed.

DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
  Gaps
  Chen D., Simon R.P., Chen J.; "Cloning of rat bimEL and bimL, and their differential expression in
   Hsu S.Y., Lin P., Hsueh A.J.W.;
"BOD (Bcl-2-related ovarian death gene) is an ovarian BH3 domain-containing prospoptotic Bcl-2 protein capable of dimerization with diverse antiapoptotic Bcl-2 members.";
MOI. Endocrinol, 12:1432-1440(1998).
  ISOId=088498-1; Sequence=Displayed;
Note=Isoform BOD-S is produced by alternative initation at
Met-104 of isoform BOD-L;
  ;
  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 40, Last annotation update)
16-SEP-2003 (Rel. 40, Last annotation update)
16-OCT-2101 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, L
   SUBUNIT, AND TISSUE SPECIFICITY
  50.0%; Score 42; DB 1; Length 196; 61.5%; Pred. No. 8.6;
  SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
  Indels
  ischemia and normal rat brain."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
531C176E5F1AC9AA CRC64;
   Event=Alternative splicing; Named isoforms=3; Name=BOD-L,
  196 AA.
  2; Mismatches
   IsoId=088498-2; Sequence=VSP_000538;
   IsoId=088498-3; Sequence=VSP_000539;
   PRT;
  SEQUENCE FROM N.A. (ISOFORM BIML).
  TISSUE=0vary;
MEDLINE=98400436; PubMed=9731710;
   Event-Alternative initiation;
   (ISOFORMS BOD-L; BOD-M AND BOD-S)
22066 MW;
   FUNCTION,
  | :||||: ||||
RIAQELRRIGDEF 157
  2 RYGRELRRMSDEF 14
  (BY SIMILARITY).
ALTERNATIVE PRODUCTS:
   Conservative
   STANDARD;
  SEQUENCE FROM N.A.,
196 AA;
  Local Similarity
  NCBI_TaxID=10116;
  088497;
   Name=BimL;
   .
ω
  145
SEQUENCE
   Query Match
   BIM_RAT
  Matches
   RESULT (
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  mitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
FUNCTION: STEREOSPECIFIC COMDENSATION OF PHOSPHORNOLEYRUVATE (PEP)
AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
   SEQUENCE FROM N.A.

MEDLINE-2225349; PubMed=1348717;

Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.H.;

"Cloning, primary structure and regulation of the ARO4 gene, encoding the tyroSine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";

Gene 113:67-74(1992).
   Doignon F., Biteau N., Aigle M., Crouzet M.; "The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative
   Gaps
   01-0CT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
FC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
  Membrane; Alternative initiation.
  BČL2-LIKE PROTEIN 11, ISOFORM BOD-L. BCL2-LIKE PROTEIN 11, ISOFORM BOD-S. FOR ISOFORM BOD-S.
   Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
   .
0
   /FTId=VSP_000539.
E -> D (IN REF. 1; AAC23594).
B4D2146F9C0B37A0 CRC64;
  DB 1; Length 196;
   3; Indels
   Missing (in isoform BOD-M).
  Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
   Missing (in isoform BimL). /FTId=VSP_000538.
   370 AA
  Score 42; DB Pred. No. 8.6;
   Mismatches
   Saccharomyces cerevisiae (Baker's yeast).
  Aljinovic G., Pohl F.M., Pohl T.M.;
   MEDLINE=94078675; PubMed=8256522;
   EMBL; AP065432; AAC23594.1; --
EMBL; AF136927; AAD26594.1; --
InterPro; IPP000712; Bell BH.
PROSITE; PS01259; BH3; FALSE_NEG.
  Alternative splicing;
  BH3
   7;
EMBL; AF065431; AAC23595.1; -. EMBL; AF065431; AAC23593.1; -.
  22055 MW;
  50.0%;
61.5%;
   ARO4 OR YBR249C OR YBR1701
  145 RIAQELRRIGDEF 157
   2 RYGRELRRMSDEF 14
   Conservative
   STANDARD;
  dUTPase in a yeast.";
Yeast 9:1131-1137(1993).
   196
196
104
160
   [2]
REVISIONS TO 205-207
   196 AA;
   Similarity
8; Conserv
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   NCBI_TaxID=4932;
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STANDARD;
   Local Similarity
  20
103
  HSSP; P29590;
  GVK1_HALN1
  CONFLICT
  Query Match
  ZN_FING
  ZN_FING
   DOMAIN
   GVK1_HALN1
  Matches
  RESULT 9
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   .;
0
  Q13049; Q9NQPB;
01-NOV-1997 (Rel. 35, Created)
15-8FEB-2003 (Rel. 41, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
2inc-finger protein HT2A (72 Pa Tat-interacting protein) (Tripartite motif-containing protein 32).
   Gaps
  SEQUENCE FROM N.A. MEDLINE-95297135; PubMed=7778269; Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.; Indentification of a novel human zinc finger protein that specifically interacts with the activation domain of lentiviral Tat
   MEDLINE-22388257; PubMed-12477932; StraubSerg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sheumen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-phosphate + H(2)0.
ENZYME REGULATION: INHIBITED BY TYROSINE.
PAPHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
  GG; GG: 0003849; F:2-dehydro-3-deoxyphosphoheptonate aldolase ...
InterPro: IRR06519; AroFGH.
InterPro: IRR06519; DAPPL/KDSA.
Pfan: PR00793; DAPPL-Synth_1; 1.
ProDom: PD005060; AroFGH; 1.
TIGRFAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
   ;
  INDUCTION: By amino acid starvation.
SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
   50.0%; Score 42; DB 1; Length 370; 43.8%; Pred. No. 17;
  Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
   ري
د ز
  653 AA.
   4; Mismatches
   PRT;
  85 QEYALRIKKLSDELKG 100
   EMBL, X61107; CAA43419.1; -. BMBL, L20296; AA656607.1; -. EMBL, 236118; CAA85212.1; -. PIR; S38185; S38185. HSSP; P00886; 1QR7.
   1 ORYGRELRRMSDEFEG 16
   proteins.";
Virology 209:347-357(1995).
  Best_Local Similarity 43.8 Matches 7; Conservative
  STANDARD;
  (Human)
   SGD; S0000453; ARO4
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   first step
   TRIM32 OR HIZA
  Homo sapiens
   TISSUE=Skin;
  HT2A_HUMAN
  Query Match
  Sehra H.
  RESULT 8
HT2A_HUMAN
  δž
   qq
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   0;
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Schentz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial manlysis of more than 15,000 full-length
human and mouse cDNA sequences.";
  Gaps
   ;
0
  min, 00.0005634; C:nucleus; TAS.
GO; GO:0003713; F:transcription co-activator activity; TAS.
   DB 1; Length 653;
   103 133 B BOX-TYPE.
27 27 F -> I (IN REF. 1).
653 AA; 71988 MW; D83B1595CA8378FD CRC64;
   -!- SIMILARITY: Contains 1 RING-type zinc finger.
   113 AA.
   Mismatches
  Score 42;
Pred. No.
   POLY-ALA
   PRT;
   InterPro; IPR00158; NHL.
InterPro; IPR00158; NHL.
InterPro; IPR001015; Znf_Bbox.
InterPro; IPR001041; Znf_ring.
Pfam; PF004436; NHL; 5.
Pfam; PF00643; Zf-ShC4; 1.
Pfam; PF00067; Zf-ShC4; 1.
SWART; SW00186; BBOX; 1.
SWART; SW00184; RING; 1.
PROSTITE: PS5119; ZF_BBOX; 1.
   PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Zinc-finger; Nuclear protein.
  EMBL; AL133284; CAB92723.1; -. EMBL; BC003154; AAH03154.1; -.
   50.0%;
61.5%;
  EMBL; U18543; AAA86474.1; -.
  Genew; HGNC:16380; TRIM32.
MIM; 602290; -.
  186 QEYGHEERRVQDE 198
   1 QRYGRELRRMSDE 13
  8; Conservative
   INTESTINE AND COLON.
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Gaps

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   STRAIN=MSEB / DSM 3109;
STRAIN=MSEB / DSM 3109;
STRAIN=MSEB / DSM 3109;
BIEDLINE-29287315; bubMed-10360571;
Welson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Reischmann R.D., Bisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Flyidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
   phospho-D-gluconate.
-!- PATHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY: 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
  -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
  -i- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-PHOSPHOGLUCONATE.
   9BOFD07EE01E60C3 CRC64;
  30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
Thermotoga maritima.
   48.8%; Score 41; DB 1;
40.0%; Pred. No. 14;
   220 AA.
   322 AA
  (Rel. 12, Created)
(Rel. 12, Last sequence update)
   6; Mismatches
       Mismatches
  InterPro; IPR006148; Gluc_gal_isom.
InterPro; IPR00590; Phosphogluconiac.
Pram: PF01182; Glucosamine_iso; 1.
TIGREAMS; TIGR01198; pgl; 1.
   PRT;
  PRT;
       4;
  EMBL; AE001772; AAD36230.1; -.
  25325 MW;
  Hydrolase; Complete proteome
   ::| ||:| :|:|
113 EKYEREIRSATDQFD 127
  40.0%;
  1 QRYGRELRRMSDEFE 15
  1 ORYGRELRRMSDEFE 15
   64
   6; Conservative
  :| ||:|: || || 50 ERLGRQLQALEDELE
   STANDARD;
    7; Conservative
  STANDARD;
  PIR; F72289; F72289.
  220 AA;
  Local Similarity
  NCBI_TaxID=2336;
   FIGR; TM1154;
  SNF4_YEAST
P12904;
01-OCT-1989 (
01-OCT-1989 (
  6PGL_THEMA
  SEQUENCE
  Query Match
  09X0N8;
   RESULT 11
SNF4_YEAST
  6PGL_THEMA
   Matches
       Matches
   RESULT 10
   Best
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   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   STRAINE-RRC-1; PLASMID-PNRC200;
MEDLINE-20504483; PubMed=11016950;
NG WI., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
NG WI., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Rhardt H., Lowe T.M., Liang P., Riley W., Hood L., DasSarma S.;
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99063795, PubMed-9847077;
MEDLINE-99063795, PubMed-9847077;
NG W.V., Ciudo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,
Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.;
Snapshot of a large dynamic replicon in a halophilic archaeon:
megaplasmid or minichromsome?";
Genome Res. 8:1131-1141(1998).
  STRAIN-NRC-817; PLASMID-PHH1;
MPDINE-92066812; PubMed-1956294;
HOTHE M., Englert C., Wimmer C., Pfeifer F.;
"A DNA region of 9 kbp contains all genes necessary for gas vesicle
  STRAIN-NRC-1; PLASMID=pNRC100;
MEDLINE=91323716; PubMed=1864501;
Jones J.G., Young D.C., Dassarma S.;
"Structure and organization of the gas vesicle gene cluster on the Halobacterium halobium plasmid pNRC100.";
   37pK protein 1.
(GVPK11 OR GVPK OR VNG5021G) AND (GVPK12 OR VNG6021G).
   Synthesis in halphilic archaebacteria.";
Mol. Microbiol. 5:1159-1174(1991).
-!- FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS
  DB 1; Length 113; 7;
  Pfam, PF05121, GvpK, 1.
Gas vesicle; Plasmid; Complete proteome.
SEQUENCE 113 AA, 12695 MW; 97A469D2C1643ABF CRC64;
   Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 110 (Halobacterium sp. (strain NRC-817). Hashaid pNRC100, plasmid pNRC200, and plasmid pHH1. Archaea; Buryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Halobacterium.
P24375; Q9HI26;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
  Score 41;
Pred. No.
  EMBL; AF016485; AAC82801.1; -. EMBL; AE005141; AAG20718.1; -.
  48.8%;
  EMBL; M58557; AAA98188.1; -.
   EMBL; X55648; CAA39178.1;
PIR; T08234; T08234.
   NCBI_TaxID=64091, 148370;
  3ene 102:117-122(1991).
  VESICLE SYNTHESIS.
  Query Match
Best Local Similarity
  SECUENCE FROM N.A.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
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Gaps

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Indels

.; 3;

Length 220;

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NCBI_TaxID=28985;
   SNF4_KLULA
                                  DOMAIN
SEQUENCE
   SEQUENCE
   Query Match
  DOMAIN
DOMAIN
  DOMAIN
      DOMAIN
   RESULT 12
SNF4_KLULA
   PSMR_ARCFU
   RESULT 13
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   EMBL; M21760; AAA34472.1; -.
EMBL; M30470; AAA35061.1; -.
EMBL; 27687; CAAA6823.1; -.
EMBL; D16506; BAA03958.1; -.
PIR; A38906; RGBYC3.
SGD; S00030851; SIRCY
GO; GO:0005634; Circtels: IDA.
GO; GO:0005634; Circtels: IDA.
GO; GO:00030295; F:protein kinase activator activity; IGI.
GO; GO:0006387; P:regulation of transcription from Pol II pro. .; IGI.
InterPro; IPR000644; CBS_domain.
  SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBURIT FAMILY.
SIMILARITY: Contains 4 CBS domains.
  SEQUENCE FROM N.A. MEDLINE-89006284; PubMed-3049255; Schueller H.-J., Entlan K.-D.; Molecular A.-T., Entlan K.-D.; "Molecular characterization of yeast regulatory gene CAT3 necessary for glucose derepression and nuclear localization of its product."; Gene 67:247-257(1988).
   SEQUENCE FROM N.A.
MEDILINE-90097921; PubMed=2481228;
MEDILINE-90097921; PubMed=2481228;

"Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae:
evidence for physical association of the SNF4 protein with the SNF1
   MEDIMES-94131988; PUDNEd-7905477; Mitchelhill K.I., Stapleton D., Gao G., House C., Michell B., Katsis F., Witters L.A., Kemp B.E., "Mammalian AMP-activated protein kinase shares structural and functional homology with the catalytic domain of yeast Snfl protein
   J. Biol. Chem. 269:2361-2364(1994).
  GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL
  Carbohydrate metabolism; Transcription regulation; Nuclear protein;
   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
   Lauguin G.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
  Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
   Saccharomycetales; Saccharomycetaceae; Saccharomyces
                           Nuclear protein SNF4 (Regulatory protein CAT3).
SNF4 OR CAT3 OR YGL115W.
16-OCT-2001 (Rel. 40, Last annotation update)
  RELATIONSHIP TO THE PROTEIN-KINASE SNF1.
   44
  Mol. Cell. Biol. 9:5045-5054(1989).
  CBS 1
   SEQUENCE OF 30-34 AND 316-322
  SEQUENCE OF 1-21 FROM N.A.
   SMART; SM00116; CBS; 4.
  Pfam; PF00571; CBS; 4.
   Repeat; CBS domain.
  SEQUENCE FROM N.A.
  protein kinase.
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   Doi A.,
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   Tomasini L., Ferrero I., Goffrini P.;

Tomasini L., Ferrero I., Goffrini P.;

Subnitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN CAUGES EXPRESSION OF GLUCOSE-REPRESSIBLE GENES UPON GLUCOSE DEPRIVATION. II INTERACTS AND HAS FUNCTIONAL RELATIONBHE TO THE PROTEIN-KINASE SNF! (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLear (By similarity).

-!- SUBCELLULAR: DOCATION: NUCLear (By similarity).
  Gaps
  Gaps
  Carbohydrate metabolism; Transcription regulation; Nuclear protein;
   Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
  ;
0
  ;
0
   DB 1; Length 322;
21;
   Length 328;
  Indels
  Indels
   DC9ED3F85E46BAD3 CRC64;
  51B387E346EE9561 CRC64;
  ..
   DB 1; ; 21;
  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear protein SNF4.
  328 AA.
   398 AA.
  Mismatches
  Mismatches
   Score 41;
Pred. No. 2
   Score 41;
  SUBUNIT FAMILY.
   Pred. No.
CBS 3.
   CBS 1.
CBS 2.
CBS 3.
CBS 4.
   PRT;
  PRT;
   EMBL; AJ277480; CAB89520.1; -.
InterPro; IPR000644; CBS_domain.
246 CB
318 CB
36401 MW;
  PSMR_ARCFU STANDARD; F
028303;
15-JUL-1998 (Rel. 36, Created)
   37163 MW;
   48.8%;
   48.8%;
   258 GEALMRRSDDFEG 270
  264 GEALMRRSDDFEG 276
  4 GRELRRMSDEFEG 16
   4 GRELRRMSDEFEG 16
  Conservative
  Conservative
  STANDARD;
   94
180
252
324
  Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
  Ouery Match
Best Local Similarity
8; Conserve
192 2
259 3
322 AA;
  Repeat; CBS domain.
DOMAIN 40
   328 AA;
   Best Local Similarity
Matches 8; Conserv
  SEQUENCE FROM N.A.
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   ä
   Darmer D., Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;
"Prinary Structure of the precursor for the sea anemone neuropeptide
Antho-RFamide (<dlu-(31-487-Phe-NH2).";
Proc. Natl. Acad. Sci. U.S.A. 88:2555-2559(1991).
-!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
NEUROMUSCULAR SYNAPSES.
-!- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.
   Gaps
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   Ĥ
                             Calliactis parasitica (Sea anemone).
Makaryota, Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nynantheas; Hormathiidae; Calliactis.
NCBI_TaxID-6114;
   AMIDE (AMIDE (AMIDE (
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  DB 1; Length 334;
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AMIDATION (G-277 PROVIDE AM
AMIDATION (G-228 PROVIDE AM
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  438E182C736EB583 CRC64;
   4;
   ANTHO-RFAMIDE.
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ANTHO-RFAMIDE.
   Neuropetide; Amidation; Repeat; Signal.
SIGNAL 126 POTENTIAL.
PRPTTDR 117 120 ANTHO-REAMIDE.
   ANTHO-REAMIDE
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  ANTHO-REAMIDE
   26;
   2; Mismatches
  ANTHO-RFAMIDE
  Score 40.5;
   Pred. No.
       Antho-RFamide neuropeptides precursor
   MEDLINE=91172845; PubMed=1706527;
   39781 MW;
  EMBL; M59166; AAA27878.1; -.
  48.2%;
  56.2%;
  PIR, A39172; A39172.
InterPro; IPR002544; FARP.
Pfam; PF01581; FARP; 15.
   9; Conservative
   266
275
284
334 AA;
   Query Match
Best Local Similarity
Matches 9: Conserv
  SEQUENCE FROM N.A.
   SEQUENCE
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  STRAIN-VC-16 / DSM 4304 / ArCC 49558;
STRAIN-VC-16 / DSM 4304 / ArCC 49558;
STRAIN-VC-16 / DSM 4304 / ArCC 49558;
MEDLINE-9804943; Pubmd-9389475;
RA Florian R.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Retchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., McKenney K., Adams M.D., Loftus B.,
Rirhanss E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Rirhanss E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Roverbeek R., Gooayne J.D., Weldman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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   This SWISS-PROT entry is copyright. It is produced through a collaboration
  Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteasome-activating nucleotidase (Proteasome regulatory subunit).
   "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:384-370(1264).
-!- FUNCTION: Required for the APP- or CPP-dependent degradation
proteins, but not small peptides, by the 20S proteasome (By
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0
   Fred. No. 26; Williams 198; Mineral 198;
  Indels

similarity).
-!- SUBUNIT: Homohexamer (Potential).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.

   182 189 ATP (POTENTIAL).
398 AA; 44964 MW; F3293BB7D6A646B4 CRC64;
   Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
   Last sequence update)
Last annotation update)
   PRT; 334 AA.
  SMART, SM0382, AAA, 1.
TIGREAMS, TIGR01242, 26Sp45; 1.
PROSITE; PS00674; AAA, 1.
Proteasome, ATP-binding; Complete proteome.
   2; Mismatches
  48.8%; Score 41;
  HAMAP, WE_00553; -; 1.
InterPro; IPR005937; 26S_p45.
InterPro; IPR003993; AAA_ATPase.
InterPro; IPR003993; AAA_ATPase_centr.
InterPro; IPR003960; AAA_ATPase_centr.
Pfam; PF00004; AAA, 1.
  Created)
  EMBL; AE000967; AAB89280.1; -.
   57.1%;
  2 RYGRELRRMSDEFE 15
  RYEREVRELRSEVE 56
  8; Conservative
  STANDARD;
   Archaeoglobus fulgidus.
   (Rel. 29, (Rel. 29, 1) (Rel. 29, 1)
   PIR; G69496; G69496.
   Query Match
Best Local Similarity
   NCBI_TaxID=2234;
   PAN OR AF1976
  TIGE; AF1976;
  FMRA_CALPA

Q01133;

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   PARTIAL SEQUENCE (ANTHO-RPAMIDE).

BEDILINE-87092339; PubMed-2879288;

Grimmellkhuijzen C.J.P., Graff D.;

"Isolation of pyroglu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide
  Schnutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P., "Identification of a novel type of processing sites in the precursor for the sea anemone neuropeptide Antho-RFamide (\langle \text{Glu-Gly-Arg-Phe-NF2} \rangle)
  AMIDE GROUP).
AMIDE GROUP).
AMIDE GROUP).
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AMIDE GROUP).
   GROUP).
  16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 40, Last sequence update)
Antho-Reamide neuropeptides type 2 precursor.
Anthopheura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nymantheea; Actiniidae; Anthopheura.
   Proc. Natl. Acad. Sci. U.S.A. 83:9817-9821(1986).
-!- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
NEUROMUSCULAR SYNAPSES.
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   (G-294
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(G-310
(G-326
   AMIDATION (G-238
AMIDATION (G-246
   or send au.

EMBL; M99170; AAA27739.1; -
Pfam, PF01581; FARP; 14.
Neuropeptide; Amidation; Repeat; Signal.

1 22 POTENTIAL.

22 ANTHO- REPAMIDE.
   ANTHO-REAMIDE
ANTHO-REAMIDE.
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ANTHO-REAMIDE.
ANTHO-REAMIDE.
   429 AA.
   ANTHO-RFAMIDE.
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  ANTHO-RFAMIDE ANTHO-REAMIDE
  ANTHO-RFAMIDE
   AMIDATION AMIDATION
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   from Anthopleura elegantissima.";
J. Biol. Chem. 267:22534-22541(1992).
   PRT;
   -:- SUBCELLULAR LOCATION: Secreted.
   SEQUENCE FROM N.A. MEDLINE=93054550; PubMed=1429603;
  |||||| : | ||:|
RYGREFQGRFGREFQG 111
   RYGRELR-RMSDEFEG 16
   STANDARD;
   from sea anemones.";
   FMR2_ANTEL
Q16994;
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  Gaps
AMIDATION (G-334 PROVIDE AMIDE GROUP).
AMIDATION (G-340 PROVIDE AMIDE GROUP).
AMIDATION (G-350 PROVIDE AMIDE GROUP).
7C54F5C606D537F4 CRC64;
  Ξ,
   Length 429;
  Indels
   Score 40.5; DB 1;
Pred. No. 34;
3; Mismatches 3;
   Search completed: September 15, 2003, 17:23:00 Job time : 4.77143 secs
  50564 MW;
   |:||||: | ||:|
212 RFGRELQGREGREFQG 227
  48.2%;
56.2%;
  2 RYGRELR-RMSDEFEG 16
   Conservative
  333
346
359
372
  Query Match
Best Local Similarity
Matches 9; Conserva
  333
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429 AA;
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@8gtn2 oryza sativ
@8gvq4 oryza sativ
@8gvq4 oryza sativ
@91grf oryza sativ
@91grf oryza sativ
@95sw6 oryza sativ
@8ryw0 oryza sativ
@8ryw0 oryza sativ
@8w315 oryza sativ
@8w315 oryza sativ
              Q995v2 neurospora
Q94h58 oryza sativ
Q8s6j1 oryza sativ
Q97i40 clostridium
  286850 mus musculu
Q8cfnl mus musculu
Q8cfnl mus musculu
Q9ayg6 oryza sativ
Q9ayg6 oryza sativ
Q8fn2 oryza sativ
Q9tn2 oryza sativ
Q9xem4 oryza sativ
   Q85609 oryza sativ
Q94hul oryza sativ
Q957a7 oryza sativ
Q9vsml drosophila
  ó
   Q81m44 oryza sativ
Q8f646 leptospira
  Q8tj31 methanosarc
   Q9vsm2 drosophila
   MEDLINE-20373792; PubMed=10917738;
MEDLINE-20373792; PubMed=10917738;
MEDLINE-20373792; PubMed=10917738;
Menes with homology to mammalian apoptosis regulators identified in zebrafish.";
Ed. Death Differ. 7:509-510(2000).
EMBL; AF231017; AAF66962.2; -...
HSSP; Q92934; 1G5J.
ZFIN; ZDB-GENB-000616-1; bad.
SEQUENCE 146 AA; 16546 MW; 28A5650BB5107ECB CRC64;
  BAD.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brazyota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
   Gaps
  ;
0
   72.6%; Score 61; DB 13; Length 146; 66.7%; Pred. No. 0.028; ive 5; Mismatches 0; Indels
  Last sequence update)
Last annotation update)
  216 AA.
   146 AA
  ALIGNMENTS
  Q9LGR6
Q9SSW6
Q9SRW0
Q8RTN5
Q8RTN5
Q8LSS
Q9USM2
Q9VSM2
Q94HU1
Q957A7
Q9VSM1
Q9VSM1
   Created)
             Q9P5V2
Q94H58
                                      098671
097140
081M44
088646
080850
080601
086107
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  Q9LGR7
Q8LHG3
  Q9XEM4
Q8GVG4
   PRT;
  PRT;
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   ::||::|||||||||||||||| KKYGQQLRRMSDEFD 107
  01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2002 (TrEMBLrel. 22,
  1 ORYGRELRRMSDEFE 15
   Conservative
 PRELIMINARY;
  PRELIMINARY;
  Similarity
10;
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   Query Match
Best Local 9
  Q9KZC5
Q9KZC5;
  Q919N2;
   09I9N2
  Best Loc
Matches
   RESULT 2
Q9KZC5
ID Q9KZCA
   RESULT 1
 Q9I9N2
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  QΫ́
  Q8xxs6 ralstonia s
Q8ytv3 oryza sativ
Q8ytv3 oryza sativ
Q989r4 rhizobium 1
Q8es55 oceanobacil
Q9ruk9 deinococcus
Q8kuf5 actinosynne
Q9kuf7 pseudomonas
Q9y86 oryza sativ
Q9n911 leishmania
Q9n911 leishmania
Q9rgx3 pseudomonas
Q9n911 leishmania
Q9rgx3 pseudomonas
Q8ei34 shewanella
Q8etil pyrobaculum
   Q9i9n2 brachydanio
   streptomyce
  September 15, 2003, 17:17:31 ; Search time 17.3714 Seconds
(without alignments)
237.680 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Description
   09kzc5
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
  Potal number of hits satisfying chosen parameters:
   830525 seqs, 258052604 residues
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
  Q919N2
Q9KZC5
Q8XXS6
Q9FV20
Q8GTN3
Q989R4
Q8KGY8
Q8ES55
  Q8KUF5
Q9HUS7
Q93X86
Q9N9N1
  Q8EI34
Q8ZTI1
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   Q9KGW3
   sp_virus:*
sp_vertebrate:*
sp_unclassified:*
   sp_invertebrate:*
   1 ORYGRELRRMSDEFEG 16
   sp_bacteriap:*
sp_archeap:*
   sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
   sp_organelle:*
  Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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  sp_rodent:*
   sp_rvirus:*
   US-09-544-664-28
  sp_mammal:*
sp_mhc:*
  sp_phage:*
sp_plant:*
  Length DB
   SPTREMBL_23:*
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Match
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1111...
114...
   Scoring table:
  Perfect score:
  Score
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Result Ñ. a

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Ambulatus, Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandlar M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Siguier M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Siguier P., Thebault P., Whalen M., Worker P., Evy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
BMBL; AL64607; Cabl5739.1; -.
InterPro; IPR003593; ABA_Arpase.
InterPro; IPR003493; ABA_Arpase.
From PF00005; ABC_transporter.
   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
  STRAIN-cv. Zhaiyeqing 8; TRANSPOSON-unspecified; TISSUE-Shoot; YF F., Zhang A., Zhang F., Chen S.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL, ARZ59976; AAG15480.1; ·.
   Score 45; DB 10; Length 567;
Pred. No. 52; 2; Mismatches 2; Indels
   Transferase.
; BD4F47AB33A685BE CRC64;
  230 AA; 25231 MW; 7C3FDA1E7A19A2A4 CRC64;
  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative GAG-POL precursor.
   53.6%; Score 45; DB 16; 64.3%; Pred. No. 20;
  567 AA.
   PRT; 1696 AA.
   1; Mismatches
  ProDom; PD000006; ABC_transporter; 1. SMART; SM00382; AAA; 1.
   Oryza sativa (indica cultivar-group)
  PRT;
                             STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
  .,
.,
   RNA-directed DNA polymerase; T
SEQUENCE 567 AA; 64419 MW;
  53.6%;
  InterPro; IPR002156; RNaseH. InterPro; IPR000477; RVTse.
   | :|:|: |: || | 547 YRQEVRKLEDKFEG 560
   | || ||| |||| ||||
168 QEIGRTLRRLVDEF 181
   Query Match
Best Local Similarity 50.08;
The Conservative
  1 QRYGRELRRMSDEF 14
   3 YGRELRRMSDEFEG 16
  Pfam; PF00075; rnaseH; 1. Pfam; PF00078; rvt; 1.
   9; Conservative
  PRELIMINARY;
   PRELIMINARY;
   Best Local Similarity
        SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  Complete proteome.
  NCBI_TaxID=39946;
  Gramene; Q9FV20;
   Polyprotein.
  SEQUENCE
   Query Match
   Q8GTN3;
  Q9FV20
   OBGTN3
  Matches
   RESULT 4
  RESULT 5
   Q9FV20
  Q8GTN3
        g
   g
  QΣ
  ã
   ;
0
   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
  SEQUENCE FROM N.A.

STRAIN=A2(2) / M145;

MEDLINE=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T.,

Cronin A., Fraser M., Goble A., Hidalgo J., Hornsby T.,

Rablnowitsch E., Rieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
   Gaps
   "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939129; Ca889025-1; -.
InterPro; IPR003265; Endo_3c.
Pfam; PF00730; HAH-GPD; 1.
   ó
  Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Ralstoniaceae, Ralstonia.
   Streptomyces coelicolor.
Bacteria; Actinobacteridae; Actinomycetales;
  56.0%; Score 47; DB 16; Length 216; 50.0%; Pred. No. 8.7;
   Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
  Indels
  Saunders D.C., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
   DDD7C717D60F7AA7 CRC64;
  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable ATP-binding ABC transporter protein.
RSC2037 OR RS03602.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical profein SCO6964.
SCO6964 OR SC6F7.17C.
  э;
Э
   Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
   230 AA.
  5; Mismatches
   Complete proteome.
   PRT;
  STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
   216 AA; 23810 MW;
   :|:| :|||: || :|
109 ERWGGDLRRLRDEADG 124
   1 ORYGRELRRMSDEFEG 16
   Local Similarity 50.0 hes 8; Conservative
   PRELIMINARY;
   Hypothetical protein;
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   NCBI_TaxID=305
   STRAIN=A3(2);
   STRAIN=A3(2);
   Hopwood D.A.;
   SEQUENCE
  Query Match
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Gaps

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08XXS6

RESULT Q8XXS6

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Best Loc Matches

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Gaps

; 0

Length 230; 4; Indels 3

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Gaps
  Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
Brust G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.,
"Comparative sequence analysis of the symbiosis island of
Mesorhizobium loti strain R?A.",
J. Bacteriol. 184:3086-3095(2002).
EMBL; ALG72112; CAD31464.1; -.
InterPro: IPR03655; SUWO_protease.
Pfam; PF02902; Peptidase_C48: 1.
PROSITE: PS50600; ULP_PROTEASE; 1.
  SEQUENCE FROM N.A.
STRAINH-HTEB31 / DSM 14371 / JCM 11309;
MEDLINE-2222077; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
  0;
  0
   53.6%; Score 45; DB 2; Length 1798; 69.2%; Pred. No. 1.8e+02; Live 1; Mismatches 3; Indels
  52.4%; Score 44; DB 16; Length 157; 50.0%; Pred. No. 19;
  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
  Ridge and its unexpected adaptive capabilities to extreme
  al protein.
1798 Aa; 196214 MW; A750A49B8C0D58lB CRC64;
  Indels
  EMEL, AP000595; BAC12744.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 157 AA; 17809 MW; 128229251596C18C CRC64;
  01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical conserved protein.
                                      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
MSI055
  Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus.
   157 AA.
   564 AA
   4; Mismatches
   Res. 30:3927-3935(2002).
                  22, Created)
22, Last sequ
   01-MAR-2003 (TrEMBLrel. 23, Created)
   Rhizobium loti (Mesorhizobium loti).
   PRT;
   PRT;
  MEDLINE-21999272; PubMed-12003951;
   : |||:|: || |
126 FSRELKRIGEEFSG 139
   ||| ||| |:| |
569 YGRLLRRFSEELE 581
  3 YGRELRRMSDEFEG 16
  3 YGRELRRMSDEFE 15
   Best_Local Similarity 50.0
Matches 7; Conservative
   Best Local Similarity 69.2
Matches 9; Conservative
   PRELIMINARY;
   PRELIMINARY;
                  01-OCT-2002 (TrEMBLrel.
  NCBI_TaxID=182710;
   SEQUENCE FROM N.A.
   environments.";
  NCBI_TaxID=381;
   Nucleic Acids
  Hypothetical
  STRAIN-R7A;
  SEQUENCE
   Query Match
   Query Match
   Q9RUK9
   Q8ES55
  RESULT 8
Q8ES55
  RESULT 9
   Q9RUK9
ID Q9
δλ
   οg
   QΫ
   g
  ;
0
   0
  STRAIN-MAPF303099,
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; MEDLINE T., Kawashima K., Kinura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Meochizuki Y., Nakayama S., Noharaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
  Gaps
   Gaps
             Oryza sativa (japonica cultivar-group).
Eukaryocka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzae; Oryzae;
   STRAIN=cv. Nipponbare;

STRAIN=cv. Nipponbare;

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,

Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vansken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Vansken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., White O., Salabberg S.L., Fraser C.M.;

"Oryas sativa chromosome 10 BAC OSJNBa0041114 genomic sequence.";

"Oryas sativa chromosome 10 BAC OSJNBa0041114 genomic sequence.";

Submitted (SEP-2002) to the RMBL/GenBank/DDBJ databases.

EMBL, AC099042; AAN08247.11. -..

EMBL, AC099042; AAN08247.11. -..
   0
   ;
0
  Score 45; DB 16; Length 1748; Pred. No. 1.7e+02; 1; Mismatches 3; Indels
  Length 1696;
  Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
NGBL_TAXID=811
   53.6%; Score 45; DB 10; Length 16: 50.0%; Pred. No. 1.7e+02; ....ma+ches 2; Indels
  2A9CE7B92C354341 CRC64;
  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein mlr6316.
  PRT; 1748 AA.
   PRT; 1798 AA.
   Hypothetical protein; Complete proteome SEQUENCE 1748 AA; 190454 MW; 2A9CE71
   Mesorhizobium loti.";
DNA Res. 7:31-338(2000).
EMBL; AP003008; BAB52630.1;
InterPro: IPR003653; SUMO_prorease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE: 1.
  53.6%;
  1341 YRQEVRKLEDKFEG 1354
   Query Match
Best Local Similarity 50.00,
7; Conservative
  3 YGRELRRMSDEFEG 16
   3 YGRELRRMSDEFE 15
  Query Match 53.6
Best Local Similarity 69.2
Matches 9; Conservative
   PRELIMINARY;
  PRELIMINARY;
  SEQUENCE FROM N.A.
   NCBI_TaxID=39947;
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Q989R4

RESULT 6 Q989R4

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Q8KGY8

RESULT 7 Q8KGY8

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   SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAOL;
STRAIN-ATCC 15692 / PAOL;
MEDIINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., H.Ckey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Gollty L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.F., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAOL, an
   Gaps
   The state of the s
  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
   ÷
   0;
   51.8%; Score 43.5; DB 2; Length 1589; 56.2%; Pred. No. 2.7e+02; tive 3; Mismatches 3; Indels 1;
   SMART; SN00304; HAMP; 1.
SMART; SN00387; HARPase_c; 1.
SMART; SN0388; Hisra, 1.
TIGRPAMS; TICR01386; cztS_silS_copS; 1.
PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PSS0041; HTH_ARRAC_FAMILY_1; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase;
  51.2%; Score 43; DB 16; Length 463; 61.5%; Pred. No. 90;
   Indels
  1589 AA; 164712 MW; 5067CF9A772A525F CRC64;
  463 AA; 50946 MW; 97FF19C2CF38006C CRC64;
  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable two-component sensor.
  463 AA.
  2; Mismatches
Pfam; PF00550; pp-binding; 1.
PROSTIE; PS50075; ACP_COMAIN; 1.
PROSTIE; PS00606; EXTOACYL_SYNTHASE; 1.
PROSTIE; PS00012; PHOSPHOPANTETHEINE; 1.
  PRT;
   Pseudomonadaceae; Pseudomonas.
  161 QNYGNR-RRVAEEFEG 175
  1 ORYGRELRRMSDEFEG 16
  | ||||| :: ||||
321 GEELRRQAEYFEG 333
  4 GRELRRMSDEFEG 16
  Best Local Similarity 56.2
Matches 9; Conservative
   Query Match
Best Local Similarity 61.5
Matches 8; Conservative
  PRELIMINARY;
  Phosphopantetheine.
   Complete proteome. SEQUENCE 463 AA;
  NCBI_TaxID=287;
  SEQUENCE
  Query Match
  PA4886
  Q9HUS7
  RESULT 11
  Q9HUS7
  δŽ
  g
  QΫ́
   g
  STAINAATCC 31555;

WEDLINE-22056096; PubMed=12060743;

YU T.W., Bai L., Clade D., Hoffman D., Toelzer S., Trinh K.Q., Xu J.,

Moss S.J., Leistner E., Floss H.G.;

"The biosynthetic gene cluster of the maytansinoid antitumor agent
ansamitocin from Actinosynnema preticsum.";

Proc. Natl. Acad. Sci. U.S.A. 99:7968-7973(2002).

EMBL; AF455501; AAM54077.1; -.

EMBL; AF455501; AAM54077.1; -.

Interpro; IPR0001227; Actransferase.

R Interpro; IPR006162; Ppantne_attach.

R Interpro; IPR006162; Ppantne_attach.

R Pfam; PF00698; Acyl_transf; 1.

R Pfam; PF00699; Acyl_transf; 1.

R Pfam; PF02801; Ketoacyl-synt. 1.
   ;
0
  Gaps
   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  0
   Actinosynnema pretiosum (subsp. auranticum).
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales;
Pseudonocardinae, Actinosynnemataceae; Actinosynnema.
NCBL_FaxID-42198;
  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
  52.4%; Score 44; DB 16; Length 564; 61.5%; Pred. No. 76; 2; Indels ive 3; Mismatches 2; Indels
  Deinococcus radiodurans,
Bacteria; Deinococcus-Thermus; Deinococcales;
Deinococcaceae; Deinococcus.
NCBL_TaxID=1299;
  InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
Pfam; PF00128; alpha-amylase; 1.
SMARY; SM00642; Aamylase; 1.
Hydrolase; Complete proteome.
SEQUENCE 564 AA; 63667 MW; B8F50B9B0DFC8D51 CRC64;
   01-OCT-2002 (TIEMBLRel. 22, Created)
01-OCT-2002 (TIEMBLRel. 22, Last sequence update)
01-MAR-2003 (TIEMBLRel. 23, Last annotation update)
                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
61ycosyl hydrolase, family 13,
   PRT; 1589 AA.
   MEDLINE-20036896; PubMed-10567266;
  Science 286:1571-1577(1999).
EMBL; AEO01983; AAF10944.1; -.
HSSP; P21332; 1UOK.
   61.5%;
  283 YVREMRRVIDEFD 295
  3 YGRELRRMSDEFE 15
  Query Match
Best Local Similarity 61.5
Matches 8; Conservative
   PRELIMINARY;
  Polyketide synthase.
   SEQUENCE FROM N.A.
  TIGR; DR1375;
   Fraser C.M.;
   STRAIN=R1;
   QBKUF5
  RESULT 10
Q8KUF5
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Gaps

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093Y86

RESULT 12

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Characterization of NADH dehydrogenases of Pseudomonas fluorescens "Characterization of NADH dehydrogenases of Pseudomonas fluorescens WCS365 and their role in competitive root colonisation.";
Submitted (JUN-2000) to the EMEL/GenBank/DDBJ databases.
EMEL; AF281148; AAF29031.1.
InterPro; IPR000283; Complex1_75K.
InterPro; IPR000144; Ferradoxin.
InterPro; IPR006565; Molybdopterin.
InterPro; IPR006565; Molybdopterin.
InterPro; IPR0011; ferz; 1...
Pfam; PR00111; ferz; 1...
  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
  Query Match 50.6%; Score 42.5; DB 2; Length 904; Best Local Similarity 56.2%; Pred. No. 2.2e+02; Matches 9; Conservative 3; Mismatches 3; Indels 1
   5; Length 5635;
SMART; SW00382; AAA; 4.
PROSTER; PS00639; THIOL_PROTEASE_HIS; 1.
ATP-binding.
SEQUENCE 5635 AA; 620050 MW; 64A9EB81A9B14641 CRC64;
   1; Indels
   Iron; Iron-sulfur.
SEQUENCE 904 AA; 98157 MW; C25E86C6D4DFA457 CRC64;
   01-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NADH dehydrogenase I, 6 subunit.
NUOS OR SO1016.
Shewanella oneidensis.
   01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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   909 AA.
   904 AA
   Pfam: PF00334; molybdopterin; 1.
Pfam: PF04879; Molybdop_Fe454; 1.
PROSITE: PS00641; COMPLEX1_75K_1; 1.
PROSITE: PS00642; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_2; 1.
   PRT;
   PRT;
  NADH dehydrogenase I subunit G.
   :||| ||||: : | |
241 ERYG-ELRRIENRFNG 255
   1 QRYGRELRRMSDEFEG 16
   Alteromonadaceae; Shewanella.
   ||:||:||| |
1535 ORFGRDLRRWS 1545
  PRELIMINARY;
   PRELIMINARY;
  Pseudomonas fluorescens.
  1 QRYGRELRRMS 11
   [1]
SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCBI_TaxID=70863;
  NCBI_TaxID=294;
   STRAIN-WCS365;
  STRAIN=MR-1;
  Q8EI34
Q8EI34;
  Q9KGW3;
   Q9KGW3
   RESULT 15
  RESULT 14
   08EI34
  Q9KGW3
   g
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    DR
DR
SQ
SQ
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  ó;
  SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
  Gaps
  L3302.02.
Lestshmania major.
Lestshmania major.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
  093386.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Entative gag-pol.
07ryza sativa (Rice).
Edwaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzeae; Oryzeae;
   "Oryga sativa chromosome 3 BAC OSJNBA0026A15 genomic sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL. AC084404, AAK50597.1; -.
Gramene; 093786; -.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve. 1.
SEQUENCE 674 AA; 75473 MW; 9FA929B1426E725E CRC64;
  ;
0
   Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,
Quail M., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
  Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
  51.2%; Score 43; DB 10; Length 674; 50.0%; Pred. No. 1.3e+02; tive 3; Mismatches 5; Indels
  Smith D.F.;
Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001593; AAA_ATPase.
InterPro; IPR00169; SHprot_acsite.
Pfam; PF03028; Dynein_heavy.
   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
  PRT; 5635 AA.
  674 AA.
  PRT;
   STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
   Dynein heavy chain, cytosolic.
   : | ||:||| |:|
258 EAYVREVRRMERNFDG 273
   1 QRYGRELRRMSDEFEG 16
  Query Match
Best Local Similarity 50.0%
  PRELIMINARY;
  PRELIMINARY;
   White O., Fraser C.M.;
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=4530;
   STRAIN=Friedlin;
  U9N9N1
   IN6N60
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RESULT 13

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OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OOONON OO

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Gaps

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RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Red T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBOY R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Medupu R., Peterson J.D., Dmayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Imprainm M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Imprainm M., Lee K., Meronald L.A.,
RA Mueller J., Khouri H., Gill J., Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
Nat. Blotechnol. 20:1118-1123(2002).
DR TICR: Sollofs -
KW Complete proteome.
SQ SEQUENCE 909 AA; 100079 MW, F71859F385BDCAC8 CRC64;
Best Local Similarity 56.2%; Pred. No. 2.2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Db 241 ERKG-ELRRENBSDEFG 16
Db 241 ERKG-ELRRENBFFG 255
```

Search completed: September 15, 2003, 17:25:48 Job time: 19:3714 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

using sw model - protein search, OM protein

September 15, 2003, 17:16:01; Search time 22.6286 Seconds Run on:

(without alignments) 112.231 Million cell updates/sec

Title: Perfect score:

US-09-544-664-29 83 1 QRYGRELRRMSDEFVD 16 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 segs, 158726573 residues Searched: 1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03;\*

| SIDS1/gcgdata\_geneseg\_genesegp\_embl\_AA1980\_DAT;\*
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| SIDS1/gcgdata\_geneseg\_genesegp\_embl\_AA1991\_DAT;\*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2100.DAT:\*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\* 221: 23: 24:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                    | Human BAD BH3 doma | Bcl2 polypeptide B | Mutant Bcl2 compet | Human Bad peptide | Mutant Bcl2 compet | Human Bad peptide | Human Bad peptide | Human Bad peptide | Human Bcl2 fluores |
|--------------------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|
| QI.                            | AAY05421           | AAB37029           | ABG78499           | AAU78626          | ABG78500           | AAU78630          | AAU78629          | AAU78628          | ABG78482           |
| EG.                            | 20                 | 21                 | 23                 | 23                | 23                 | 23                | 23                | 23                | 23                 |
| Length 1                       | <br>16             | 16                 | 20                 | 20                | 21                 | 21                | 22                | 23                | 24                 |
| Query<br>ore Match Length DB I | 100.0              | 100.0              | 100.0              | 100.0             | 100.0              | 100.0             | 100.0             | 100.0             | 100.0              |
| Score                          | 83                 | 83                 | 83                 | 83                | 83                 | 83                | 83                | 83                | 83                 |
| Result<br>No.                  |                    | 7                  | m                  | 4                 | ιΩ                 | 9                 | 7                 | 80                | σ                  |

97US-0946039. 97US-0060133.

07-OCT-1997; 26-SEP-1997;

(UNIW ) UNIV WASHINGTON

WPI; 1999-255058/21.

Korsmeyer

| Human Bad peptide | nteracting       | BC12 |     |     |     | it Bcl2 |     |     | Mutant Bcl2 compet |    | Mutant Bcl2 compet | 0        | Bc12 | Mutant Bcl2 compet | Human Bad peptide | Human Bad peptide | Human Bad peptide | Human Bad peptide | Human Bad peptide | Human Bad peptide | ರ  | ಇರ    | $\alpha$ | Human Bad peptide | d peptid | ന        | $\pi$ | Bad peptid | alian |     | protein for | -xL/Bcl- | prolif | Human BAD mutant a |
|-------------------|------------------|------|-----|-----|-----|---------|-----|-----|--------------------|----|--------------------|----------|------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----|-------|----------|-------------------|----------|----------|-------|------------|-------|-----|-------------|----------|--------|--------------------|
| AAU78605          | $\circ$ $\vdash$ | 34   | 784 | 784 | 784 | BG78487 | 784 | 34  | 784                | 24 | 34                 | ABG78493 | 84   | 84                 | 86                | 9                 | AAU78611          | 86                | 86                | 86                | 86 | 86    | 86       | O                 | 86       | AAU78620 | 86    | 984        | 963   | 703 | 324         | 557      | B135   | B703               |
| AA                | A B              | ABG. | ABG | ABG | AB  | AB      | AB  | ABG | AB                 | AB | AB                 | AB       | AB   | AB                 | AA                | AA                | AA                | ΑĄ                | AA                | Ā                 | AA | AA    | AA       | AA                | AAU      | AA       | AA    | AAU,       | AA    | AA  | AAM         | AAM      | AAB    | AA                 |
| 23                | 233              | 23   | 23  | 23  | 23  | 23      | 23  | 23  | 23                 | 23 | 23                 | 23       | 23   | 23                 | 23                | 23                | 23                | 23                | 23                | 23                | 23 | 23    | 23       | 23                | 23       | 23       | 23    | 23         | 21    | 22  | 18          | 19       | 21     | 22                 |
| 24                | 25               | 25   | 25  | 25  | 25  | 25      | 25  | 25  | 25                 | 25 | 25                 | 25       | 25   | 25                 | 25                | 25                | 25                | 25                | 25                | 25                | 25 | 25    | 25       | 25                | 25       | 25       | 25    | 25         | 26    | 26  | Θ           | 168      | Θ      | ø                  |
| 100.0             |                  | 00   | 00  | 00. | 00  |         | 00  | 00  |                    | 00 |                    |          | 00   |                    | 00.               | 0                 | 00.               |                   | 00                | 00                | 00 | 100.0 | 00       | 00                | 00       | 00       | 00    | 00         | 00    | 00  | 00.         | 00       |        |                    |
| 80 a              | ი ღ<br>დ         | 83   | 83  | 83  | 83  | 83      | 83  | 83  | 83                 | 83 | 83                 | 83       | 83   | 83                 | 83                | 83                | 83                | 83                | 83                | 83                | 83 | 83    | 83       | 83                | 83       | 83       | 83    | 83         | 83    | 83  | 83          | 83       | 83     | 83                 |
| 10                | 7 7              | 13   | 14  | 15  | 16  | 17      | 18  | 19  | 20                 | 21 | 22                 | 23       | 24   | 25                 | 26                | 27                | 28                | 29                | 30                | 31                | 32 | 33    | 34       | 35                | 36       | 37       | 38    | 39         | 40    | 41  | 42          | 43       | 44     | 45                 |

## ALIGNMENTS

RESULT 1

BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer: lymphoproliferative condition; arthritis; autoimmune disease; therapy. AAY05421 standard; peptide; 16 AA. 98WO-US19765. (first entry) Human BAD BH3 domain. Homo sapiens. W09916787-A1. 22-SEP-1998; 02-JUL-1999 08-APR-1999 AAY05421; AAY05421   $^{\circ}$ 

# X & X O O O O O O O O O O X & Q

QΨ qq

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WO200240530-A2.
   Homo sapiens.
  15-NOV-2002
  23-MAY-2002,
   Synthetic.
  ABG78499;
  Sequence
  RESULT 3
  ABG78499
        δŽ
   g
  X Y X D X D X D X D 
  5
  ;
   The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n=1-10; X=C^{-}O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X=O or OH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COH or OH 
  This sequence represents the BH3 domain of human BAD.

The invention relates to a bcl homology domain 3 (BH3 domain),
derived from a prospotite member of the BCL-2 family. The
BH3 polypeptide can be used in a method for promoting apoptosis in a
target cell, especially where the cell is a cancer cell a virus infected
cell or an autoantibody producing cell. The BH3 polypeptide can be used
in therapeutic compositions for treating disease including cancer, other
lymphoproliferative conditions, arthritis, inflammation, and autoimmune
diseases, which may result from the down regulation of cell death
  Gaps
  ρQ
  Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl_2 superfamily; BH3 domain; cell death agonis; Bad; apoptosis modulation; B cell lymphoma/leukemia 2, cancer, prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
  New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
  ó
  Length 16;
  Indels
  ö
  Score 83; DB 20;
Pred. No. 1.3e-07;
   Ζ,
  Mismatches
   ŗ
  Bcl2 polypeptide BH3 domain peptide #29.
   ŝ
   Shan
   Ā.
Bcl homology domain 3 polypeptide
  Claim 18; Page 18; 74pp; English.
  Example 1; Fig 4; 104pp; English.
  0
   AAB37029 standard; peptide; 16
   stroke; myocardial infarction.
  100.0%;
ilarity 100.0%;
Conservative 0;
   (UYJE-) UNIV JEFFERSON THOMAS
  1 ORYGRELRRMSDEFVD 16
   1 ORYGRELRRMSDEFVD 16
  06-APR-2000; 2000WO-US09352.
   99US-0128202.
   Wang J, Zhang Z,
  (first entry)
   WPI; 2000-679325/66.
  Local Similarity
wes 16; Conserv
  16 AA;
  WO200059526-Al
  Homo sapiens.
   07-APR-1999;
  28-FEB-2001
  12-0CT-2000
   requlation.
  Seguence
  AAB37029;
   Huang Z,
  Query Match
  Best Loc
Matches
   RESULT 2
   AAB37029
```

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phenyl optionally monosubstituted with a 1-56 straight or branched chain the periodes provided with a 1-56 straight or branched chain always group, or benzyl. The peptides Aa33701-B37058 represent examples of the peptide portion of the conjugate. The peptides represent amalogues of a Bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/lenkemia 2 (Bc1-2)-mediated blookage of reversing B cell lymphoma/lenkemia 2 (Bc1-2)-mediated blookage of subject afflicted with a cancer cells. It is also useful for inhibiting Bc1-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that capted so the cancer includes prostate, colorettal, gastric, on small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders acquired increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficlency syndrome (AIDS), stroke or myocardial infarction.
   ö
   This invention relates to a novel mutant protein which is derived from a wild type human BCl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flaxible loop from the wild type BCl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant BCl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the BCl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of BCl-2 to inhibit programmed cell
  New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis \cdot
   Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.
  Gaps
monosubstituted with a 1-5C straight or branched chain alkyl group,
   ô
  Length 16;
   Indels
  Mutant Bcl2 competitive binding assay peptide #16.
  100.0%; Score 83; DB 21; 100.0%; Pred. No. 1.3e-07;
  Nettesheim DG;
   Mismatches
   Example 2; Page 17; 36pp; English.
  ABG78499 standard; Peptide; 20 AA.
  .
0
  Yoon H,
  1 QRYGRELRRMSDEFVD 16
   1 QRYGRELRRMSDEFVD 16
  15-NOV-2001; 2001WO-US45693.
   20-NOV-2000; 2000US-0716395
  (first entry)
   Query Match
Best Local Similarity 100.
Matches 16; Conservative
  Fesik SW, Petros AM,
   WPI; 2002-490141/52.
   (ABBO ) ABBOTT LAB.
   16 AA;
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Matches

88866

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This invention relates to a novel mutant protein which is derived from a wild type human BCl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type BCl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant BCl-2 protein comprises a 16 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the BCl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2
   New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
   Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mutein.
   Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
  Human Bad peptide #30 which binds to a member of the Bcl-2 family.
  Mutant Bcl2 competitive binding assay peptide #17.
   100.0%; Score 83; DB 23; 100.0%; Pred. No. 1.8e-07;
   Nettesheim DG;
  Mismatches
   ABG78500 standard; Peptide; 21 AA.
   Example 2; Page 17; 36pp; English.
   AAU78630 standard; Peptide; 21 AA.
  0;
   H,
   1 ORYGRELRRMSDEFVD 16
  Yoon
  15-NOV-2001; 2001WO-US45693.
   20-NOV-2000; 2000US-0716395.
   (first entry)
   (first entry)
   peptide of the invention.
  16; Conservative
   Petros AM,
  WPI; 2002-490141/52.
   Query Match
Best Local Similarity
  (ABBO ) ABBOTT LAB
  21 AA;
  WO200240530-A2
   Homo sapiens
  Homo sapiens
   18-JUN-2002
   15-NOV-2002
   23-MAY-2002.
   Synthetic.
   Fesik SW,
  Sequence
  AAU78630;
  ABG78500;
  useful
  Matches
  AAU78630
                                       ABG78500
  RESULT
  δŽ
  쉽
   ö
   0;
   The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bol-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bol-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
  New derivatives of Bad peptide, useful for identifying compounds that bind to Bol-2 proteins, potential agents for treating cancer and
  Gaps
   Gaps
  Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
   Human Bad peptide #26 which binds to a member of the Bcl-2 family.
apoptosis. The present sequence represents a human Bcl2
  0;
   0;
  Petros AM;
   100.0%; Score 83; DB 23; Length 20; 100.0%; Pred. No. 1.7e-07;
  Length 20;
  Indels
   Indels
  Joseph MK, Olejniczak ET,
1, Matayoshi E, Zhang H;
  0;
   · (
  Score 83; DB 23;
Pred. No. 1.7e-07;
  Mismatches
   Mismatches
  ischemic injury; suppressor; BH3 domain.
  Example 1; Page 14; 31pp; English.
  AAU78626 standard; Peptide; 20 AA.
  ;
   0;
  100.0%;
100.0%;
   16
   1 QRYGRELRRMSDEFVD 16
  1 QRYGRELRRMSDEFVD 16
  1 QRYGRELRRMSDEFVD 16
   04-SEP-2001; 2001WO-US27410.
  06-SEP-2000; 2000US-0656399.
  Fesik SW, Meadows RP, Jos
Nettesheim DG, Swift KM,
   QRYGRELRRMSDEFVD
  (first entry)
   Similarity 100.
16; Conservative
   Best Local Similarity 100.
Matches 16; Conservative
                  peptide of the invention.
   degenerative disease
   WPI; 2002-292254/33.
   (ABBO ) ABBOTT LAB
  20 AA;
   20 AA;
  WO200220568-A2.
  18-JUN-2002
  Homo sapiens.
  14-MAR-2002.
  Sequence
   Seguence
   AAU78626;
   Query Match
  Query Match
   Local
```

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ğ

0

Gaps

;

Length 21; Indels

Fesik

```
The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bel-1-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bel-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
   The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bc1-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to
  is of Bad peptide, useful for identifying compounds that proteins, potential agents for treating cancer and
  New derivatives of Bad peptide, useful for identifying compounds that bill to Bcl-2 proteins, potential agents for treating cancer and
  Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
ischemic injury; suppressor; BH3 domain.
   Human Bad peptide #28 which binds to a member of the Bcl-2 family.
   Length 22;
  Indels
   ET,
H;
  ..
   Score 83; DB 23;
Pred. No. 1.9e-07;
   Joseph MK, Olejniczak
I, Matayoshi E, Zhang
  Mismatches
  AAU78628 standard; Peptide; 23 AA.
  Claim 15; Page 18; 31pp; English.
   Claim 15; Page 18; 31pp; English.
  New derivatives of Bad peptide,
  ..
   100.0%;
   1 QRYGRELRRMSDEFVD 16
   21
   04-SEP-2001; 2001WO-US27410.
   06-SEP-2000; 2000US-0656399
   Meadows RP, Jo
DG, Swift KM,
  (first entry)
  ORYGRELRRMSDEFVD
   Query Match
Best Local Similarity 100.
Matches 16; Conservative
   bind to Bcl-2 protein
degenerative disease
   degenerative disease
   WPI; 2002-292254/33.
                   WPI; 2002-292254/33.
  (ABBO ) ABBOTT LAB
  22 AA;
   WO200220568-AZ.
  bind to Bcl-2
  Homo sapiens.
  18-JUN-2002
   Fesik SW, Nettesheim I
  14-MAR-2002
  Sequence
   AAU78628;
  RESULT 8
AAU78628
QΫ
   g
  ΠX
   ó
  The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AMU78601-AMU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
   derivatives of Bad peptide, useful for identifying compounds that
  Gaps
  Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
   Human Bad peptide #29 which binds to a member of the Bcl-2 family.
  \omega_{\rm Ind} to BCL-2 proteins, potential agents for treating cancer and degenerative disease
  ó
  Petros AM;
   Petros AM;
   Length 21;
  Indels
   ET,
H;
   Fesik SW, Meadows RP, Joseph MK, Olejniczak ET, Nettesheim DG, Swift KM, Matayoshi E, Zhang H;
  .;
   Score 83; DB 23;
Pred. No. 1.8e-07;
   Meadows RP, Joseph MK, Olejniczak
DG, Swift KM, Matayoshi E, Zhang
  Mismatches
   ischemic injury; suppressor; BH3 domain.
   AA.
   Claim 15; Page 18; 31pp; English.
  ó
   AAU78629 standard; Peptide; 22
   100.0%;
ilarity 100.0%;
Conservative 0
   1 QRYGRELRRMSDEFVD 16
  21
   04-SEP-2001; 2001WO-US27410.
  06-SEP-2000; 2000US-0656399.
  04-SEP-2001; 2001WO-US27410.
   06-SEP-2000; 2000US-0656399
   6 QRYGRELRRAGDEFVD
  (first entry)
   WPI; 2002-292254/33
  Local Similarity
Les 16; Conserv
   (ABBO ) ABBOTT LAB
  (ABBO ) ABBOTT LAB
  21 AA;
   WO200220568-A2.
  Nettesheim DG,
                 WO200220568-A2
  Homo sapiens
  18-JUN-2002
  14-MAR-2002.
  14-MAR-2002
```

Sequence

Query Match

Best\_Loca

ð 셤 AAU78629;

RESULT 7

Petros AM;

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Gaps

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Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease;
ischemic injury; suppressor; BH3 domain.
  New derivatives of Bad peptide, useful for identifying compounds bind to Bol-2 proteins, potential agents for treating cancer and decementive disease -
   Human Bad peptide #5 which binds to a member of the Bcl-2 family.
   Joseph MK, Olejniczak ET,
1, Matayoshi E, Zhang H;
   Location/Qualifiers
   AA.
  Claim 4; Page 16; 31pp; English.
   AAU78605 standard; Peptide; 24
   1 ORYGRELRRMSDEFVD 16
   QRYGRELRRMSDEFVD 21
  9
                             21
   04-SEP-2001; 2001WO-US27410.
   06-SEP-2000; 2000US-0656399.
   Fesik SW, Meadows RP, Jo
Nettesheim DG, Swift KM,
                 6 ORYGRELRRMSDEFVD
  (first entry)
    QRYGRELRRMSDEFVD
   Local Similarity 100.
les 16; Conservative
  degenerative disease
  WPI; 2002-292254/33
  (ABBO ) ABBOTT LAB.
  24 AA;
   Key
Misc-difference
  WO200220568-A2
  Homo sapiens
  18-JUN-2002
   14-MAR-2002.
   Sequence
  Query Match
Best Local 9
   9
  AAU78605;
  Matches
  RESULT 10
   AAU78605
  õ
   원
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   П
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  6
  0
   This invention relates to a novel mutant protein which is derived from a wild type human BC1-2 protein. The mutant is created by replacing a sequence of amino acid residues comprishing a flathible loop from the wild type BC1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant BC1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the BC1-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of BC1-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human BC12
members of the Bcl-7 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AMU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
  New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis \,
  Human; Bc12; Bc1X1; programmed cell death; apoptosis; mutant; mutein.
  Gaps
  Gaps
  ó
  .,
  100.0%; Score 83; DB 23; Length 24; 100.0%; Pred. No. 2e-07;
  Length 23;
  Indels
  Indels
  . 2e-07;
  ó
  Score 83; DB 23;
Pred. No. 1.9e-07;
  Nettesheim DG;
  Mismatches
  Human Bcl2 fluorescein labelled peptide #2.
  Mismatches
   Example 2; Page 15; 36pp; English.
  A.
   100.08; 214
   .;
  Yoon H,
  ABG78482 standard; Peptide; 24
  100.0%;
  16
  100.08;
  15-NOV-2001; 2001WO-US45693.
  20-NOV-2000; 2000US-0716395.
  (first entry)
  1 ORYGRELRRMSDEFVD
   Best Local Similarity 100.
Matches 16; Conservative
  peptide of the invention
  Conservative
  Petros AM,
   WPI; 2002-490141/52.
  Query Match
Best Local Similarity
Matches 16; Conserv
   (ABBO ) ABBOTT LAB
   24 AA;
  23 AA;
  WO200240530-A2.
   Homo sapiens
  15-NOV-2002
  23-MAY-2002
   Synthetic.
   Fesik SW,
   Seguence
  Query Match
  Sequence
  9
  ABG78482;
  RESULT 9
   ABG78482
```

that

Petros AM;

```
ö
The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bcl-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bcl-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide, and, compared with the Bad peptide, may have better physical
   properties, particularly solubility. The present sequence represents of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
  Gaps
  ;
0
  100.0%; Score 83; DB 23; Length 24; 100.0%; Pred. No. 2e-07; ive 0; Mismatches 0; Indels
   AAU78627 standard; Peptide; 24 AA.
   RESULT 11
AAU78627
ID AAU78
```

9

```
15-NOV-2001; 2001WO-US45693.
   (CNRS ) CENT NAT RECH SCI.
  Conservative
  Edelman L, Jacotot E,
  PASTEUR.
   WPI; 2002-619260/66.
   Local Similarity
les 16; Conserv
   cancer or ischemia
  25 AA;
                       WO200261105-A2.
  WO200240530-A2.
   ISNI ( ASNI)
   sapiens.
  23-MAY-2002
   08-AUG-2002
  Synthetic.
   Synthetic.
  ABG78481;
   Sequence
  Query Match
  Best Loc
Matches
   RESULT 13
ABG78481
   Homo
  δ
  g
  .
0
   The present invention relates to new peptides that are derived from a wild-type human Bad peptide and are able to bind to a member of the Bol-2 protein family. The peptides are useful, when labelled, in competitive/displacement assays for identifying substances that bind to members of the Bol-2 family and may induce or suppress apoptosis so are potentially useful for treating cancer (inducers) or degenerative diseases or ischemic injury (suppressors). The peptides of the invention have high helix propensity, maintain the contacts of the wild-type Bad peptide and, compared with the Bad peptide, may have better physical properties, particularly solubility. The present sequence represents one of a collection of Bad peptides (AAU78601-AAU78631) that were derived from the BH3 domain of the human wild-type Bad peptide.
   Mitochondrial membrane permeabilisation; mitochondrion; PTPC; permeability transition pore complex; virucide; neuroprotective; vasctropic; cytostatic; infection; cell death regulation; apoptosis; mitochondrial permeability transition pore complex modulator; cancer; apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
   New derivatives of Bad peptide, useful for identifying compounds that
bind to Bcl-2 proteins, potential agents for treating cancer and
degenerative disease
  Gaps
   Human; Bad; Bcl-2; apoptosis; cancer; inducer; degenerative disease; ischemic injury; suppressor; BH3 domain.
   Human Bad peptide #27 which binds to a member of the Bcl-2 family.
  0
  Petros AM;
  100.0%; Score 83; DB 23; Length 24; 100.0%; Pred. No. 2e-07;
  ows RP, Joseph MK, Olejniczak BT,
Swift KM, Matayoshi E, Zhang H;
  Mismatches
  ABP56161 standard; peptide; 25 AA.
  PTPC-interacting TOX peptide #27.
   Claim 15; Page 18; 31pp; English.
  ;;
  1 QRYGRELRRMSDEFVD 16
   04-SEP-2001; 2001WO-US27410.
  2000US-0656399.
  (first entry)
                                    (first entry)
  QRYGRELRRMSDEFVD
  Local Similarity 100.
nes 16; Conservative
   WPI; 2002-292254/33.
  (ABBO ) ABBOTT LAB.
   Meadows
  24 AA;
  Nettesheim DG,
  WO200220568-A2.
   Homo sapiens
  06-SEP-2000;
  28-MAR-2003
                                    18-JUN-2002
   14-MAR-2002
   Sequence
   ABP56161;
  Fesik SW,
         AAU78627;
  Query Match
  Matches
   RESULT 12
  ABP56161
  QQ
   δŽ
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comprising at least a first functional molecule covalently linked to a second functional molecule, which is able to modulate the activity of the permeability transition pore complex (PTPC) of the mitochondria.

(I) has the function of specifically targeting and entering a tissue cell population. The second functional molecule has the function of specifically targeting and inducing or preventing the death of the cells by apoptosis by regulating the opening or the closing of the PTPC of the mitochondria or its fragment. (I) has virucide, neuroprotective, vasctropic and cytostatic activities, and can be used as a mitochondrial permeability transition pore complex (PTPC) modulator. (I) is useful for regulating call death regulatory molecules, specifically the apoptogenerative diseases, inhimant hepatitis or viral infections.

The present sequence represents a PTPC-interacting TOX peptide which is
   Human; Bcl2; BclXl; programmed cell death; apoptosis; mutant; mutein.
  New chimeric bifunctional molecules that target specific cells and regulate the apoptosis function of the permeability transition pore complex of the mitochondria, useful for treating or preventing e.g.
   The present invention describes a chimeric bifunctional molecule
  ·,
  Indels
   given in the exemplification of the present invention
  100.0%; Score 83; DB 23; 100.0%; Pred. No. 2.1e-07;
   Mismatches
   Human Bcl2 fluorescein labelled peptide #1.
   ABG78481 standard; Peptide; 25 AA.
  Briand J;
  Claim 9; Page 11; 76pp; English.
  ô
  1 ORYGRELRRMSDEFVD 16
  01-FEB-2002; 2002WO-EP01633.
  02-FEB-2001; 2001US-265594P.
   15-NOV-2002 (first entry)
```

Gaps

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This invention relates to a novel mutant protein which is derived from a wild type human Bc1-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bc1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bc1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bc1-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bc1-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bc12
  This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flatible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify aubstances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2
  New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis \,
  BclXl; programmed cell death; apoptosis; mutant; mutein
   0;
   Length 25;
  DB 23; Length 25;
   Indels
   Mutant Bcl2 competitive binding assay peptide #2.
   0
   Score 83; DB 23;
Pred. No. 2.1e-07;
   Nettesheim DG;
   Mismatches
  Score 83;
  AA.
   Example 2; Page 17; 36pp; English.
  25
   Ë
   0:
  100.0%;
  100.08;
  21
   100.0%;
   1 ORYGRELRRMSDEFVD 16
  Yoon
  ABG78485 standard; Peptide;
   15-NOV-2001; 2001WO-US45693.
   20-NOV-2000; 2000US-0716395.
  QRYGRELRRMSDEFVD
   (first entry)
  the invention.
  Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
   peptide of the invention.
  Petros AM,
   WPI; 2002-490141/52
  (ABBO ) ABBOTT LAB.
   25 AA;
  25 AA;
  WO200240530-A2.
  Human; Bcl2;
   sapiens
   15-NOV-2002
  23-MAY-2002.
  peptide of
   Synthetic.
   Fesik SW,
  ABG78485;
   Sequence
  Seguence
  Query Match
   RESULT 15
   ABG78485
ID ABG7
  888888888888888
  g
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   ó
   This invention relates to a novel mutant protein which is derived from a wild type human BC1-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type BC1-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant BC1-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the BC1-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of BC1-2 to inhibit programmed cell qeath or apoptosis. The present sequence represents a human BC12
   New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis \,
  New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis
   Human; Bc12; Bc1X1; programmed cell death; apoptosis; mutant; mutein.
   Gaps
   0;
   Length 25;
   0; Indels
  Mutant Bcl2 competitive binding assay peptide #1.
   100.0%; Score 83; DB 23; 100.0%; Pred. No. 2.1e-07;
   Nettesheim DG;
   Nettesheim DG;
   Mismatches
  ABG78484 standard; Peptide; 25 AA.
  Example 2; Page 15; 36pp; English.
   Example 2; Page 17; 36pp; English
   ;
   Ë
   Yoon H,
  1 QRYGRELRRMSDEFVD 16
  Yoon
  15-NOV-2001; 2001WO-US45693.
  20-NOV-2000; 2000US-0716395.
                          20-NOV-2000; 2000US-0716395
   (first entry)
   Best Local Similarity 100.
Matches 16; Conservative
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   Petros AM,
  WPI; 2002-490141/52.
  WPI; 2002-490141/52
  (ABBO ) ABBOTT LAB.
   (ABBO ) ABBOTT LAB.
  25 AA;
  WO200240530-A2.
   Homo sapiens.
   15-NOV-2002
   23-MAY-2002.
   SW,
   Synthetic.
   Fesik SW,
  Sequence
   ABG78484;
   Query Match
   Fesik
  RESULT 14
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0; Gaps

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APPLICATION NUMBER: US/08/665,617
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CLASSIFICATION NUMBER: US/08/665,617
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ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
RESISTRATION NUMBER: CL-8
REFERRATION NUMBER: CL-8
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 16; Conservative
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US-08-665-617-2
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   linear
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APPLICANT: Tue, Henry
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
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TITLE OF INVERTION: PROLIFERATION
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRICATION NUMBER:
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                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0421 US
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-04166
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   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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CA
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  ö
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Patent No. 5955703

GENERAL INFORMATION:

JETLIE OF INVATION:

TITLE OF INVENTION:

MURBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE:

COMPUTER:

COUNTRY:

OUTY:

San Diego

STATE:

COMPUTER:

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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
UNMER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
   0; Mismatches
   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
  US-08-985-335-1
: Sequence 1, Application US/08985335
; Patent No. 6080847
: Patent No. APPLICANT: Hillman, Jennifer L.
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acids
  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
   108 ORYGRELRRMSDEFVD 123
   1 QRYGRELRRMSDEFVD 16
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2
  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
  CITY: Palo Alto
  COUNTRY: U
ZIP: 94304
   S
US-08-717-123-2
   STATE:
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Gaps

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108 QRYGRELRRMSDEFVD 123
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acids
   1 QRYGRELRRMSDEFVD 16
  E: Diskette
IBM Compatible
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Best Local Similarity 100.
Matches 16; Conservative
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   STREET: 31/2
CTTY: Palo Alto
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  MEDical
LIBRARY: General
Topic 1683637
   GENERAL INFORMATION:
APPLICANT: Hillma
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   USA
  FILING DATE:
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   COMPUTER:
   COUNTRY:
   ; CLONE: CUS-09-410-372-7
  RESULT 6
US-09-410-372-7
   STATE:
   RESULT 7
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   Gaps
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   0;
  100.0%; Score 83; DB 3; Length 168; 100.0%; Pred. No. 2.2e-07; Live 0; Mismatches 0; Indels
   Length 168;
  0; Indels
  APPLICANT: Yue, Henry
APPLICANT: Lal, Freeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
   Query Match 100.0%; Score 83; DB 3; I Best Local Similarity 100.0%; Pred. No. 2.2e-07; Matches 16; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
  E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
  PF-0421 US
  Sequence 1, Application US/09410372
Patent No. 6281334
GENEAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
   108 QRYGRELRRMSDEFVD 123
  TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
  1 QRYGRELRRMSDEFVD 16
               LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
  LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
  Best Local Similarity 100.
 SEQUENCE CHARACTERISTICS:
  CORRESPONDENCE ADDRESS:
  LIBRARY: SYNORAB01
CLONE: 358673
   CITY: Palo Alto
  IMMEDIATE SOURCE:
  USA
   ADDRESSEE:
STREET: 31
  S
  STATE: C. COUNTRY:
   ; CLONE: 3
US-09-410-372-1
  RESULT 5
US-09-410-372-1
  US-08-985-335-7
   Query Match
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RESULT 10

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         KORSMEYER, Stanley J. WYENTION: Bcl.x/Bcl.2 ASSOCIATED CELL DEATH WVENTION: REGULATOR BCJURGES: 59
  SOFTWARE: Patentin Friedras #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NORMER: US/08/661,479
FILING DATE: 11.5UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
  COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
  STREET: 7733 FORSTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
   15726A-000700
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  88.0%; Scc
100.0%; Pr
tive 0;
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPEAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
   30,223
   NAME: Smith, William M
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
  1 QRYGRELRRMSDEF 14
   8 QRYGRELRRMSDEF 21
   LENGTH: 23 amino acids TYPE: amino acid
   14; Conservative
   STRANDEDNESS: single
                                      TITLE OF INVENTION: BC.
TITLE OF INVENTION: REG
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
  TOPOLOGY: linear
MOLECULE TYPE: peptide
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   CLASSIFICATION: 530
   CITY: Palo Alto
STATE: California
COUNTRY: US
  Query Match
Best Local Similarity
   COUNTRY: US
ZIP: 63105
   94301
   US-08-661-479-10
         APPLICANT:
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   100.0%; Score 83; DB 4; Length 168; 100.0%; Pred. No. |2.2e-07;
   Query Match 88.0%; Score 73; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 1.5e-06; Matches 14; Conservative 0; Mismatches 0; Indels
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   US-08-333-565-10

Sequence 10, Application US/08333565

Sequence 10, Application US/08333565

GENERAL INFORMATION:

APPLICANT: KORSMETER, Stanley J.

TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

IIILE OF INVENTION: REGULATOR
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWN APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-OCT-1994
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 15726A-000700
TELEPHONE: (415) 326-242
INFORMATION FOR EQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
  NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
TOWNSENCE TOWNSENCE AND TOWNSENCE AND CLEW
STREET: 379 Lytton Avenue
  Mismatches
CURRENT FILING DAIE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOFWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
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US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 584209
GENERAL INFORMATION:
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  108 ORYGRELRRMSDEFVD 123
   1 ORYGRELRRMSDEFVD 16
  1 QRYGRELRRMSDEF 14
  8 ORYGRELRRMSDEF 21
  Conservative
  STRANDEDNESS: single TOPOLOGY: linear
   MOLECULE TYPE: peptide
   ; TYPE: PRT; ORGANISM: Homo sapiens US-09-375-257-2
  STREET: 379 Lytton
CITY: Palo Alto
STATE: California
   Best Local Similarity
Matches 16; Conserv
   ns
  COUNTRY: U
   US-08-333-565-10
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Gaps

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Sequence 57, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: BERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
  APPLICANT: KORSMEYDER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
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  Length 59;
  COMPUTER REGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-FOS/MS-DOS
SOFRWARE: Patentin Release #1.0, Version #1.30
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION WUMBER: US/08/733,505A FILING DATE:
   4.2e-06;
hes 0;
   88.0%; Score 73; DB 2;
100.0%; Pred. No. 4.2e-0
ive 0; Mismatches
  ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI COUNTRY: USA
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   US-08-733-505A-58; Application US/08733505A; Patent No. 5856445; Patent INFORMATION:
  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35.197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 57:
   1 QRYGRELRRMSDEF 14
   Query Match
Best Local Similarity 100.
Matches 14; Conservative
   SEQUENCE CHARACTERISTICS:
  LENGTH: 59 amino acids
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   STREET: 7733 FOR CITY: ST. LOUIS STATE: MISSOURI
   COUNTRY: US
  63105
  US-08-733-505A-57
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   Gaps
   APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBGRITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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   88.0%; Score 73; DB 2; Length 59; 100.0%; Pred. No. 4.2e-06; tive 0; Mismatches 0; Indels
  88.0%; Score 73; DB 2; Length 59; 100.0%; Pred. No. 4.2e-06;
   0; Indels
  MEDIUM TYPE: Floppy disk
COMPTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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   100.0%; Pred. ...
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  ADDRESSE: HOWELL & HAFERKAMP, L.C. STREET: 773 FORSTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI
  US-08-733-505A-56
; Sequence 56, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
  965458
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFRX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHRARACTERISTICS:
ILBNGTH: 59 amino acids
   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DORALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELEFORMUNICATION INFORMATION:
TELEFORM: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
  1 QRYGRELRRMSDEF 14
   46 QRYGRELRRMSDEF 59
  1 ORYGRELRRMSDEF 14
  46 QRYGRELRRMSDEF 59
   LENGTH: 59 amino acids TYPE: amino acid
  Conservative
   14; Conservative
  TOPOLOGY: linear
MOLECULE TYPE: peptide
   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-56
  COMPUTER READABLE FORM:
  amino acid
   Best Local Similarity
Matches 14; Conserv
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Matches 14; Conserv
  STRANDEDNESS:
   STRANDEDNESS
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   US-08-733-505A-55
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   Query Match
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RESULT 15
US-08-661-479-2
Sequence 2, Application US/08661479
Fatent No. 58342008
Fatent No. 58342008
FAPLICANT: KORSHEYER, Stanley J.
APPLICANT: KORSHEYER, Stanley J.
TITLE OF INVENTION: BGJLATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: APPLICANCE ADDRESS:
STREET: 379 Lytton Avenue
CITY: Palo Alto
STREET: CITY: Palo Alto
CITY: Palo Alto
STREET: CIT ALIA ALIA
  88.0%; Score 73; DB 2; Length 204; 100.0%; Pred. No. 1.6e-05; tive 0; Mismatches 0; Indels
  Score 73; DB 1; Length 204;
Pred. No. 1.6e-05;
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OTHER INFORMATION: /note= "Deduced amino acid sequence OTHER INFORMATION: of mouse BAD."
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OCHRITE: IEM PC compatible
OCHRITE: PETCODY MS-DOS
SOFTWARE: Petchtin Release #1.0, Version #1.25
CURRENT APPLICATION NORM: US/08/661,479
FILIND BATE: 11-7UN-1995
  FILING DATE: 11-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/33,565
FILING DATE: 31-OCT-1994
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION: INFORMATION:
   Search completed: September 15, 2003, 17:45:06 Job time: 8.34286 secs
  Query Match 88.0%; Scc
Best Local Similarity 100.0%; P:
Matches 14; Conservative 0;
  TELEPHONE: (415) 326-2400
TELEPAK: (415) 326-442
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
   1 ORYGRELRRMSDEF 14
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Best Local Similarity 100.
Matches 14; Conservative
  TOPOLOGY: linear MOLECULE TYPE: protein
  NAME/KEY: Protein
  US-08-661-479-2
             US-08-333-565-2
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   Sequence 2, Application US/08333565
Patent NO. 5622862
CENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCES: 59
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
  /note= "Deduced amino acid sequence of mouse BAD."
  Query Match 88.0%; Score 73; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 4.2e-06; Matches 14; Conservative 0; Mismatches 0; Indels
   COUPTER READABLE FORM:

MEDIUM TYPE: Rhoppy disk

MEDIUM TYPE: Rhoppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Rhoppy disk

COMPUTER: BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/33,565

ATTORNEY/AGENT UNFORMATION:

MAME: SMICH, WAILIAM M

REGISTRATION NUMBER: 15726A-000700

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATIO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
  965458
  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REPERENCE/POCKET UNMBER: 9654;
TELECOMMUNICATION INFORMATION:
TELEPRONE: (314) 727-5188
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERICTICS:
LENGTH: 59 amino acids
  1 ORYGRELRRMSDEF 14
   46 ORYGRELRRMSDEF 59
   STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: peptide
   MOLECULE TYPE: protein
  NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION:
OTHER INFORMATION:
  linear
  TYPE: amino acid STRANDEDNESS:
  US-08-733-505A-58
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   US-08-333-565-2
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Gaps

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   Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
  1 QRYGRELRRMSDEFVD 16
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
  US-09-544-664-29
83
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Match Length DB
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  Scoring table:
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  8833
770
770
770
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770
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  Database :
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   Searched:
   Run on:
  5482760987654321
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Sequence 258, Applications of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co US-09-922-378-2 US-09-894-657-1 US-09-894-657-1 US-09-922-378-3 US-09-922-378-3 4 US-10-066-179-3 4 US-10-106-179-3 5 US-10-156-761-9145 5 US-10-156-761-9145 5 US-09-815-242-13003 US-09-815-242-13003 US-09-815-242-5312 US-09-815-242-5312 US-09-815-242-5312 US-09-815-242-5312 US-09-815-242-5312 0.0001 100000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0

RESULT 2 US-09-922-378-2

| Sequence 13424, App. Sequence 13424, App. Sequence 13594, Appl. Sequence 40, Appl. Sequence 10330, Appl. Sequence 61, Appl. Sequence 62, Appl. Sequence 7241, App. Sequence 7241, App. Sequence 241, App. Sequence 10, Appl. Sequence 12, Appl. Sequence 123, Appl. | PF 7                                                                                                                    |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------|
| US-10-198-070-6 US-242-13 US-10-166-087-14 US-10-166-087-14 US-10-166-087-14 US-10-166-087-14 US-10-166-087-14 US-10-166-087-18 US-10-166-087-18 US-10-10-186-087-18 US-10-186-087-186-087-18 US-10-186-087-186-087-18                                                                                                                                              | US-09-70-244-394<br>US-09-940-244-394<br>US-09-950-510-25<br>US-09-712-363-205<br>US-10-156-761-146<br>US-09-950-510-12 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                         |
| 126<br>126<br>127<br>127<br>127<br>127<br>127<br>127<br>127<br>127<br>127<br>127                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1 W W W 4 4                                                                                                             |
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| 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                         |

#### ALIGNMENTS

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   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: EDELMAN, IERA

APPLICANT: DECOTOY, ETIENNE DANIEL FRANCOIS

APPLICANT: BELLAND, JEBA-PAIL

TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET

TITLE OF INVENTION: PUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX

TITLE OF INVENTION: (PPC)

TITLE OF INVENTION: (PPC)

TITLE OF INVENTION: (PPC)

CURRENT APPLICATION NUMBER: US/10/059,261

CURRENT APPLICATION NUMBER: 60/265,594

PRIOR PELING DATE: 2001-02-02

PRIOR PILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 325
   Gaps
  ó;
  OTHER INFORMATION: Description of Unknown Organism: TOX peptide
  100.0%; Score 83; DB 15; Length 25; 100.0%; Pred. No. 5.3e-07; ive 0; Mismatches 0; Indels
REGULT 1
US-10-059-261-258
Sequence 258, Application US/10059261
Publication No. US20030077826A1
   1 ORYGRELRRMSDEFVD 16
   6 QRYGRELRRMSDEFVD 21
   Query Match
Best Local Similarity 100.0*
""+nhes 16; Conservative
  SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 258
LENGTH: 25
  ORGANISM: Unknown Organism
  US-10-059-261-258
   TYPE: PRT
   FEATURE:
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Gaps

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Length 168;
   Length 168;
  Indels
  Indels
   Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARB: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
RAPPLICATION NUBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
   100.0%; Score 83; DB 9; I
100.0%; Pred. No. 3.9e-06;
tive 0; Mismatches 0;
   100.0%; Score 83; DB 9; L
100.0%; Pred. No. 3.9e-06;
ive 0; Mismatches 0;
   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
  SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-894-657-7
                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-894-657-1
  APPLICANT: Hillman, Jennifer L.
  TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
   INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CERRACTERISFICS:
LENGTH: 168 amino acid
TYPE: amino acid
   US-09-894-657-7; Sequence 7, Application US/09894657; Patent No. US20020096569Al GENERAL INFORMATION:
   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
   STRANDEDNESS: single
   108 QRYGRELRRMSDEFVD 123
  108 ORYGRELRRMSDEFVD 123
  1 QRYGRELRRMSDEFVD 16
  1 QRYGRELRRMSDEFVD 16
   Yue, Henry
Lal, Preeti
Shah, Purvi
   NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
   LIBRARY: GenBank
CLONE: 1683637
   TOPOLOGY: linear IMMEDIATE SOURCE:
   Query Match
Best Local Similarity 100.0
Matches 16; Conservative
  Conservative
  CITY: Palo Alto
STATE: CA
      CLONE: 358673
  USA
   Query Match
Best Local Similarity
Matches 16; Conserva
  COUNTRY:
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   Gaps
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  APPLICANT: BOTHER, Milliam A.
APPLICANT: BOTHER, Tilman
APPLICANT: Ollersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
  Length 168;
   Query Match 100.0%; Score 83; DB 9; Length 16 Best Local Similarity 100.0%; Pred. No. 3.9e-06; Matches 16; Conservative 0; Mismatches 0; Indels
   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM. DOS
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,657
FILING DATE: 28-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/410,372
  Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL.
PROLIFERATION
   ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
   REFERENCE/DOCKET NUMBER: PF-0421 US
  FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy
REGISTRATION UUMBER: 36,749
  Sequence 1, Application US/09894657
Patent No. US20020098559A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
Sequence 2, Application US/09922378 Patent No. US20020037869A1
  STRANDEDNESS: single
  1 QRYGRELRRMSDEFVD 16
   Yue, Henry
Lal, Preeti
Shah, Purvi
  COMPUTER READABLE FORM:
  LIBRARY: SYNORAB01
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES: 9
  TOPOLOGY: linear IMMEDIATE SOURCE:
   TYPE: amino acid
  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-378-2
   COUNTRY: USA
   ZIP: 94304
  STATE: CA
   GENERAL INFORMATION:
  LENGTH: 168
   RESULT 3
US-09-894-657-1
   SEQ ID NO 2
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Gaps

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US-10-174-105A-147

Sequence 147, Application US/10174105A

Publication No. US2030068652A1

GENERAL INPORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: CARN, Michael J.
APPLICANT: TAN, YI
TILLE OF INVENTION: CONTEXT: INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHI
FILE REFERENCE: CST-138 CIP3 CIP3
FILE REFERENCE: CST-138 CIP3
CURRENT APPLICATION NUMBER: US/10/174,105A
  LOCATION: (8)...(8); OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated US-10-174-105A-147
  Gaps
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  Length 204;
  Ouery Match 67.5%; Score 56; DB 15; Length 15; Best Local Similarity 100.0%; Pred. No. 0.0084; Matches 11; Conservative 0; Mismatches 0; Indels
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   Score 70; DB 14; L/Pred. No. 0.00064;
   1; Mismatches
  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
   CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29
   CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
   PRIOR APPLICATION NUMBER: US 09/148,712 PRIOR FILING DAIE: 1998-09-04 PRIOR APPLICATION NUMBER: US 09/535,364 PRIOR FILING DAIE: 2000-03-24
  ; Sequence 9145, Application US/10156761; Publication No. US20030119018a1; GENERAL INFORMATION:
   OTHER INFORMATION: Synthetic Peptide
  APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
   84.3%;
  NUMBER OF SEQ ID NOS: 193
SOFWRARE: Patentin version 3.1
SEQ ID NO 147
LENGTH: 15
   ORGANISM: Artificial Seguence
  145 ORYGRELRRMTDEF 158
   1 QRYGRELRRMSDEF 14
   Conservative
  4 GRELRRMSDEF 14
   1 GRELRRMSDEF 11
                                 ; ORGANISM: Mus musculus US-10-066-179-3
   Query Match
Best Local Similarity
' hes 13; Conserve
   NAME/KEY: MOD_RES
   US-10-156-761-9145
  TYPE: PRT
  FEATURE:
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  Sequence 3, Application US/09922378
Patent No. US2020023869A1
GENERAL INFORMATION:
APPLICANT: HORDE, William A.
APPLICANT: HOLDE, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HOMEN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE REFERENCE: 480140.428D3
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2011-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
   Sequence 3, Application US/10066179
Publication No. US20020115631A1
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HOMAN BAD POLYBEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HOMAN BAD POLYBEPTIDES, ENCODING NUCLEIC
FILE REPERENCE: 480140.428C1
CURRENT APPLICATION NUMBER: US/10/066,179
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
US-10-066-179-2
; Sequence 2, Application US/10066179
; Publication No. US20020115631A1
; GENERAL INFORMATION:
APPLICANT: HORNE, William A.
; APPLICANT: Oltersdorf, Tilman A.
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND WETHODS OF USE
; FILE REFERENCE: 480140.428C1
; CURRENT APPLICATION NUMBER: US/10/066,179
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
   Length 168;
   84.3%; Score 70; DB 9; Length 204; 92.9%; Pred. No. 0.00064; live 1; Mismatches 0; Indels
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   1 QRYGRELRRMSDEFVD 16
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US-09-922-378-3
  US-10-066-179-2
   SEQ ID NO 2
  Query Match
  SEQ ID NO 3
  LENGTH:
  Matches
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   APPLICANT: AMERICAN ACCOUNTS AND HE HOWARD
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DATA
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-05-37
PRIOR FILING DATE: 2000-01-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
   50.6%; Score 42; DB 9; Length 810; 61.5%; Pred. No. 1.1e+02; tive 3; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-36
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER: 05-257,931
PRIOR FILING DATE: 2001-02-16
NUMBER: 05-257,931
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PRIOR FILING DATE: 2001-02-16
NUMBER: 05-257,931
   NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13003
LENGTH: 876
   ; Sequence 13003, Application US/09815242; Patent No. US20020061569A1
ENERGAL INFORMATION:
APPLICANT: Haselbeck, Robert
  APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
  ) ORGANISM: Staphylococcus aureus US-09-815-242-12636
  ; ORGANISM: Staphylococcus aureus US-09-815-242-13003
  Query Match
Best Local Similarity 61,5%;
Conservative
3, Conservative
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185 GRELPILADEYVD 197
   4 GRELRRMSDEFVD 16
   US-09-815-242-13003
   SEQ ID NO 12636
  TYPE: PRT
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  Score 44; DB 15; Length 215;
Pred. No. 12;
3; Mismatches 2; Indels
  50.6%; Score 42; DB 15; Length 647; ilarity 57.1%; Pred. No. 83; Conservative 1; Mismatches 5; Indels
   APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
   CHARGE OF THE CATE  APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKANA, UUN
APPLICANT: ISHIKANA, UUN
APPLICANT: SHIBA, TADATOSHI
APPLICANT: SHIBA, TADATOSHI
APPLICANT: SAKAKI, YOSHITUVII
APPLICANT: BARAKI, YOSHITUVI
APPLICANT: HATTORI, MASHHRA
TIILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: 299-262
CURRENT APPLICATION NUMBER: US/10/156,761
   CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
  US-09-815-242-12636; Sequence 12636, Application US/09815242; Patent No. US20020061569A1
  Sequence 9735, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
   PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
   TYPE: PRT , ORGANISM: Streptomyces avermitilis US-10-156-761-9145
   ; ORGANISM: Streptomyces avermitilis US-10-156-761-9735
  APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
  53.0%;
61.5%;
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9445
LENGTH: 215
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  Query Match
Best Local Similarity 61.35
   1 ORYGRELRRMSDE 13
   APPLICANT: OMURA, SATOSHI
   Query Match
Best Local Similarity
2, Conserva
  GENERAL INFORMATION:
  RESULT 10
US-10-156-761-9735
   TYPE: PRT
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  Query Match 49.4%; Score 41; DB 15; Length 312; Best Local Similarity 50.0%; Pred. No. 57; Matches 8; Conservative 3; Mismatches 5; Indels
  Length 312;
   5; Indels
  49.4%; Score 41; DB 15; 50.0%; Pred. No. 57;
  APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: BARIBA, HROSHI
APPLICANT: BSHBA, TABAYOSHI
APPLICANT: SHIBA, TABAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: J02-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
SRIOR FILING DATE: 2001-05-30
SRIOR FILING DATE: 2001-05-30
SRIOR FILING DATE: 2001-05-30
SRO ID NO 7867
SEQ ID NO 7867
  3; Mismatches
  Search completed: September 15, 2003, 17:47:53 Job time : 13.6857 secs
; CURRENT FILING DATE: 2002-05-29
; PRICR APPLICATION NUMBER: JP 2001-204089
; PRICR FILING DATE: 2001-05-30
; PRICR APPLICATION NUMBER: JP 2001-272697
; PRICR FILING DATE: 2001-08-02
; NOWBER OF SEQ ID NOS: 15109
; SEQ ID NO 7630
; LENGTH: 312
   Sequence 7867, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7630
  ; ORGANISM: Streptomyces avermitilis US-10-156-761-7867
  | | | ||: |:|
125 QLSGEERRRIIDDFMD 140
  | | | ||: |:|:|
125 QLSGEERRRLIDDFMD 140
  1 QRYGRELRRMSDEFVD 16
  1 QRYGRELRRMSDEFVD 16
   Query Match
Best Local Similarity 50.0%
   APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
  RESULT 15
US-10-156-761-7867
   TYPE: PRT
  g
   δŏ
  d
  .;
0
  Gaps
  Score 42; DB 9; Length 879;
Pred. No. 1.1e+02;
3; Mismatches 2; Indels
  APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Tramancto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
   FILE REFERENCE: ELITRA, 011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,931

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-16

SEQ ID NOS: 14110
  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
IITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERBENE: 249-262
   CURRENT APPLICATION NUMBER: US/10/156,761
  .; LOCATION: (1)...(879)

COTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-5312
  Sequence 7630, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
  Sequence 5312, Application US/09815242 Patent No. US20020061569A1
   ORGANISM: Staphylococcus aureus
   50.6%;
61.5%;
   ISHIKAWA, JUN
HORIKAWA, HIROSHI
  GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                ||||| ::||:||
251 GRELPILADEYVD 263
   255 GRELPILADEYVD 267
  4 GRELRRMSDEFVD 16
4 GRELRRMSDEFVD 16
  Query Match 50.6
Best Local Similarity 61.5
Matches 8; Conservative
  APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
   NAME/KEY: VARIANT
   RESULT 14
US-10-156-761-7630
   US-09-815-242-5312
   APPLICANT:
APPLICANT:
   TYPE: PRT
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September 15, 2003, 17:16:55 ; Search time 3.77143 Seconds
(without alignments)
199.507 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
   127863 seqs, 47026705 residues
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   US-09-544-664-29
83
1 QRYGRELRRMSDEFVD 16
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
  SwissProt_41:*
   Title:
Perfect score:
Sequence:
  Scoring table:
  Database :
   Searched:
   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|           | Description    | 2934 homo sapien | 337.  | 035147 rattus norv | 4918 mus musculu |      | 83j4 rhizobium l |       | P79023 candida alb |       |       | 5886 trypanosoma |      |       |      |      | 3525 reovirus (t |      | Q8xfc4 salmonella |      | Q8tpf7 methanosarc |      | 1931 bacillus st |      |      | Q9hv01 pseudomonas |      |      |      | σ    | 7514  | 5392      | fka7     | 2257 escherichia |
|-----------|----------------|------------------|-------|--------------------|------------------|------|------------------|-------|--------------------|-------|-------|------------------|------|-------|------|------|------------------|------|-------------------|------|--------------------|------|------------------|------|------|--------------------|------|------|------|------|-------|-----------|----------|------------------|
| SUMMARIES | ID             | BAD HUMAN 092    | MOUSE |                    | SE               |      | IIFO             | HUMAN | CANAL              | YEAST | SCOLI | TRYCR            |      | SORBU |      |      |                  | -    |                   |      |                    |      |                  |      |      |                    |      |      |      |      | MYCGE | _MYCPN P7 | ECOL6 08 | TIG_ECOLI P2     |
|           | DB             | ; -              | Н     | Н                  | П                | Н    | Н                | Н     | -                  | Н     |       |                  | Н    | ~     | Н    | H    | Н                | Н    | _                 | Н    | Н                  | Н    |                  |      |      |                    |      |      |      |      | Н     | -         | Η,       | -                |
|           | Length         | 168              | 204   | 205                | 196              | 196  | 457              | 653   | 370                | 861   | 261   | 380              | 429  | 631   | 220  | 365  | 418              | 418  | 432               | 503  | 545                | 545  | 880              | 1967 | 172  | 468                | 87   | 185  | 198  | 251  | 384   | 0         | 432      | 432              |
| οN        | Query<br>Match |                  | 88.0  | 88.0               | 50.6             | 50.6 | 50.6             | 50.6  | 49.4               | 49.4  | 48.2  | 48.2             | 48.2 | 48.2  | 47.0 | 47.0 | 47.0             | 47.0 | 47.0              | 47.0 | 47.0               | 47.0 | 47.0             | 47.0 | 46.4 | 46.4               | 45.8 | 45.8 | 45.8 | 45.8 | 45.8  | 45.8      | 45.8     | 45.8             |
|           | Score          | 83               | 73    | 73                 | 42               | 42   | 42               | 42    | 4.1                | 41    | 40    | 40               | 40   | 40    | 39   | 39   | 39               | 38   | 39                | 39   | σ<br>(۳            | 99   | 39               |      | 38.5 | w                  | 38   | 38   | 38   | 38   | 38    | 38        | 38       | 38               |
|           | Result<br>No.  |                  | 7     | М                  | 4                | រោ   | 9                | 7     | 8                  | Q     | 10    | 11               | 12   | 13    | 14   | 15   | 16               | 17   | 18                | 19   | 20                 | 21   | 22               | 23   | 24   | 25                 | 26   | 27   | 28   | 29   | 30    | 31        | 32       | 33               |

| Q9n0w2 b alpha-(1, | Q9byc5 h alpha-(1, | P79282 s alpha-(1, | Q816y4 arabidopsis | P34703 caenorhabdi | Q18823 caenorhabdi | P24117 mycoplasma | P75728 escherichia |            | Q55587 synechocyst |            | Q49640 mycobacteri |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|------------|--------------------|------------|--------------------|
| FUT8_BOVIN         | FUT8_HUMAN         | FUT8_PIG           | EMF2_ARATH         | EMB5_CAEEL         | LML1_CAEEL         | DP3B_MYCCA        | UBIF_ECOLI         | PSMR_ARCFU | Y335_SYNY3         | BAR1_HUMAN | RELA_MYCLE         |
| Н                  | Н                  | Н                  | Н                  | H                  | <del>-</del> -1    | Н                 | <del>,-</del> 1    | М          | н                  | Ч          | Н                  |
| 575                | 575                | 575                | .631               | 1521               | 1535               | 375               | 391                | 398        | 481                | 777        | 787                |
| 45.8               | 45.8               | 45.8               | 45.8               | 45.8               | 45.8               | 44.6              | 44.6               | 44.6       | 44.6               | 44.6       | 44.6               |
| 38                 | 38                 | 38                 | 38                 | 38                 | 38                 | 37                | 37                 | 37         | 37                 | 37         | 37                 |
| 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                 | 42         | 43                 | 44         | 45                 |

## ALIGNMENTS

| R.SIII.II  |                                                                                                                                              |
|------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| 340        | ad_Human<br>ID Bad_Human Standard; PRT; 168 AA.                                                                                              |
| 255        | C 092934; 014803;<br>T 01-W07-1997 (Rel: 35, Created)                                                                                        |
| 3 5 5 E    | 10-UCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)                                                    |
| 188        | 5                                                                                                                                            |
| <br>       | DAN VA BOOK ON BULLING.<br>HOMO Sapiens (Human)<br>Booksavingts, Motsavis, Character, Vartabrats, Butalanetemi.                              |
| 3 2 2      | Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.<br>NCRI marTh=9606.                                                               |
| S S S      | 1007 0007                                                                                                                                    |
| RA E       | SEQUENCE FROM N.A. Yin D.X., Li Z., Huang B., Chen S., Zhou H.;                                                                              |
| 2 5        | "A numan protein that interacts with BCI-2 and have homology to mouse<br>BAD.";                                                              |
| IZ 8       | Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.                                                                                     |
| Z CL       | [2]<br>SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.                                                                                     |
| X 6        | MEDLINE=97083574; PubMed=8929532;                                                                                                            |
| ₹ E        | wang n6., kapp u.k., keed J.C.;<br>"Bcl-2 targets the protein kinase Raf-1 to mitochondria.";                                                |
| RI         | Cell 87:629-638(1996).                                                                                                                       |
| χ γ.<br>σ. | [3]<br>SEOUENCE FROM N.A.                                                                                                                    |
| RA to      | Takayama S., Reed J.C.;                                                                                                                      |
|            | submitteed (Oct-1997) to the Embijoembann/DDD databases.                                                                                     |
|            | SEQUENCE FROM N.A., AND DIMERIZATION.                                                                                                        |
| RC.        | TISSUE=Bone marrow;                                                                                                                          |
| X A        | MEDLINE~98049554; PubMed=9388232;<br>O+tilie S . Diaz T -T. Horne W. Chang T. Wang Y., Wilson G.                                             |
|            | , , , , ,                                                                                                                                    |
|            | "Dimerization properties of human BAD.";                                                                                                     |
| Z a        | J. Biol. Chem. 272:30866-30872(1997).                                                                                                        |
|            | SEQUENCE FROM N.A.                                                                                                                           |
| 2          | TISSUE=Lung;                                                                                                                                 |
| X K        | MEDLINE=2238825/; Pubmed=124//952;<br>C+romshovn D I Doinnold D A Cromso I H horne I C                                                       |
| RA         | Strausberg N.D., Ferngord E.S., Wagner L., Shenmen C.M., Schuler G.D.,                                                                       |
| RA         | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,                                                                            |
| RA<br>DD   | Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hslen F.,<br>Diatchenko I. Marusina K. Barmer A.A. Rubin G.M. Hong I.                  |
| RA.        | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,                                                                        |
| RA         | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,                                                                           |
| KA<br>Ra   | kaha S.S., Loquettano N.A., Peters G.J., Abramson K.J., Muttany S.J.,<br>Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., |
| R.         | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,                                                                        |
| RA<br>RA   | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,<br>Fahov I. Helton R. Ketteman M. Madan A. Rodrimses S. Sanchez A.             |
| RA.        | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,                                                                              |
| RA         | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,                                                                                     |

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  SIMILARITY: Contains 1 Bc1-2 homology 3 (BH3) domain.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 64 and 91.
  MEDELNE-21073561; PubMed=11206074; Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
  (BY
  PHOSPHORYLATION (BY PKA AND PKB) (BY
  PHOSPHORYLATION (BY PKA AND PKB) (BY
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
  PKB)
  Phosphorylation; Polymorphism; 3D-structure
  PKA
  60; 60:0005737; C:cytoplasm; NAS.
60; 60:0005741; C:mitochondrial outer membrane; NAS.
60; 60:0005515; F:protein binding activity; NAS.
60; 60:0008632; P:apoptotic program; TAS.
60; 60:0008631; P:induction of apoptosis; NAS.
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   SIMILARITY).
PHOSPHORYLATION (BY
   SIMILARITY
  EMBL; U66879; AAB36516.1; ALT_FRAME.
   InterPro; IPR000712; Bc12_BH.
PROSITE; PS01259; BH3; FALSE_NEG.
   BH3
   EMBL; AF021792; AAB72092.1; -. EMBL; AF031523; AAB88124.1; -. EMBL; BC001901; AAH01901.1; -.
  STRUCTURE BY NMR OF 103-127
   124
  9
  118
   HGNC:936; BAD.
  PDB; 1G5J; 07-FEB-01.
  similarity).
  75
  66
  118
   Fesik S.W.;
  MIM; 603167
   Apoptosis;
  MOD_RES
  MOD_RES
  MOD_RES
   Genew;
```

```
ó
  14.37 proceins and survival kinases cooperate to inactivate bath by most cell 6:41-51(2000).

15. Cell 6:41-51(2000).

16. Cell 6:41-51(2000).

17. FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2.

16. Submary: Forms heterodimers with the anti-apoptotic proteins, Bcl-2 and Bcl-w. Also binds protein 5100AlO (By similarity).

17. Submary: Forms heterodimers with the anti-apoptotic proteins. Bcl-3 and bcl-w. Also binds protein 5100AlO (By similarity).

18. Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.

19. DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

19. Subsequent phosphorylation on Ser-112 in response to survival stimuli.

19. Subsequent phosphorylation on Ser-1136 promotes heterodimerization.
   TISSUE-Brain, and Thymus;
MEDLINE-95136361; PubMed=7834748;
Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
Bad, a heterodiameric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
Cell 80:285-291(1995).
  with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-155, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-136 is the major site of AKYPKB phosphorylation, Ser-155 the major site of protein kinase A (CAPK) phosphorylation.
  Gaps
  ķά
  PHOSPHORYLATION, AND NUTAGENESIS OF SER-112 AND SER-136.
MEDLINE-9802383; PUDMed-9381178;
Del Peso L., Gonzalaez-Garcia M., Page C., Herrera R., Nunez G.;
"Interleukin-3-induced phosphorylation of BAD through the protein
   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Muxinae; Mus.
  "14-3-3 proteins and survival kinases cooperate to inactivate BAD
  Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,
Greenberg M.E.;
  .
0
  01-Nov-1997 (Rel. 35, Created)
01-Nov-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
BC12-antagonist of cell death (BAD) (BC1-2 binding component
  Length 168;
  0; Indels
                       A -> S (in dbSNP:3729933).
   121
18392 MW; 69FD8D27DDEE3241 CRC64;
  100.0%; Score 83; DB 1; 1 100.0%; Pred. No. 1.8e-06;
  /FTId=VAR_015380.
   6) (Bcl-xL/Bcl-2 associated death promoter). BAD OR BBC6.
  204 AA
  Mismatches
SIMILARITY).
  MUTAGENESIS OF SERINE RESIDUES.
MEDLINE=20403302; PubMed=10949026;
  0;
   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
  108 ORYGRELRRMSDEFVD 123
  1 QRYGRELRRMSDEFVD 16
   Science 278:687-689(1997).
  Conservative
  STANDARD;
   Mus musculus (Mouse).
  168 AA;
   Similarity
  SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
                     107
  16;
  kinase Akt.
  BAD_MOUSE
  SEQUENCE
  Query Match
Best Local
                       VARIANT
   HELIX
  Matches
  RESULT 2
```

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interaction with Bcl-w in sympathetic neurons.";
  Apoptosis;
  SEQUENCE
   Query Match
   VARSPLIC
   CONFLICT
   PROSITE;
  MUTAGEN
  MOD_RES
  MOD_RES
  MUTAGEN
   DOMAIN
  HSSP;
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   ö
   PHOSPHORYLATION (BY PRA AND PKB).
PHOSPHORYLATION (BY PRA AND PKB).
PHOSPHORYLATION (BY PRA AND PKB).
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
S->A: NO PHOSPHORYLATION.
BCL.X(L).
  Hsu S.Y., Kaipia A., Zhu L., Hsueh A.J.W.;
"Interference of BAD (Bc1-xL/Bc1-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
  D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator BAD in the rat brain.";
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
   Gaps
  MEDLINE-21109372; PubMed=11161472; Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.; Functional characterization of two splice variants of rat BAD and
   ..
O
  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
BCl2-antagonist of cell death (BAD) (BCl-2 binding component 6) (Bcl-xL/BCl-2 associated death promoter).
  Score 73; DB 1; Length 204; Pred. No. 9e-05; 0; Mismatches 0; Indels
  SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137
SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
   6C2BA910205053F7 CRC64;
  SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
   205 AA.
  MEDLINE=98194755; PubMed=9535132;
   PIR; A55671; A55671.
HSSP; Q92934; 1G5J.
MGD; MG1:1096330; Bad.
InterPro; IPR000712; Bc12_BH.
PROSITE; Pc01259; BH3; FALSE_NEG.
Apoptosis; Phosphorylation.
   MEDLINE=98034386; PubMed=9369453;
   Neurosci. Lett. 243:137-140(1998).
   22080 MW;
   100.0%;
   EMBL; L37296; AAA64465.1; -.
  88.0%;
   1 QRYGRELRRMSDEF 14
  14; Conservative
  STANDARD;
  Rattus norvegicus (Rat).
   035147; 070256; Q9JHX1;
  161
112
136
136
136
  204 AA;
   SEQUENCE FROM N.A.
   Local Similarity
  NCBI_TaxID=10116;
   TISSUE=Brain;
   rissum=Brain;
  TISSUE=Ovary;
   SEQUENCE
  Query Match
   MOD_RES
MOD_RES
  MOD_RES
  BAD_RAT
   MUTAGEN
   MUTAGEN
  MUTAGEN
  DOMAIN
  Matches
   RESULT
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"ISSUE SPECIFICITY: Expressed in all tissues tested, including brain, liver, spleen and heart. In the brain, restricted to epithelial cells of the choroid plexus. Isoform alpha is the more abundant form.

-!-DOMAIN: Intact Blaid domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

-!-DAMAIN: Intact Blaid domain is required by BIK, BID, BAK, BAD AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

Subsequent phosphorylation on Ser-113 in response to survival stimuli. Subsequent phosphorylation on Ser-137 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-166, a site within the BH3 domain. leading to the release of Bcl-x(L) and the promotion of cell survival.
  LPRPKSAGTATQMRQSASWTRIIQSWWDRNLGKGGSTPSQ
-> EELTYSYEFLPVRAIAMEGWPLLWSFQSFPHTLPPTPP
EVAMFPLRYWTALRRLC (in isoform Beta).
   NO EFFECT ON HETERODIMERIZATION
  S->A: NO HETERODIMERIZATION WITH 14-3-3
   /FTIG=VSP_000534.
S->A: NO EFFECT ON HETERODIMERIZATION
WITH 14-3-3 PROTEINS.
  (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
(BY SIMILARITY).
  major site of protein kinase A (CAPK) phosphorylation (By
   PHOSPHORYLATION (BY PKA AND PKB)
   (BY SIMILARITY).
PHOSPHORYLATION (BY PKA AND PKB)
   WITH BCL2 NOR WITH PROTEIN P11.
SDAGGR -> ERRGRK (IN REF. 1).
7AFA71DAE9CF4A81 CRC64;
  DB 1; Length 205;
   -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
  PS01259; BH3; FALSE_NEG.
  Event=Alternative splicing; Named isoforms=2;
   IsoId=035147-1; Sequence=Displayed;
  PROTEINS.
   Score 73;
  EMBL; AF003523; AAC53374.1; -. 
EMBL; AF031227; AAC15100.1; -. 
EMBL; AF279910; AAF91427.1; -. 
EMBL; AF279911; AAF91428.1; -.
   34 SI
22228 MW;
   Bcl2_BH.
  88.08;
   113
   137
  156
   205
   InterPro; IPR000712;
   29
205 AA;
  Q92934; 1G5J
  similarity).
  156
   137
   166
   113
  137
   Name=Beta;
   Name=Alpha
```

```
Query Match
Best Local Similarity
  BIM_RAT
  Matches
   RESULT 5
   ŏ
   a
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                               ó:
   ISOId=054918-3; Sequence=VSP_000537;
TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B-AND T-LYMPHOID CELL
  SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOX,
  BAX OR BAK (BY SIMILARITY).
SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES.
ALTERNATYE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                     Gaps
   O'Connor L., Strässer A., O'Reilly L.A., Hausmann G., Adams J.M.,
Cory S., Huang D.C.S.;
"Bim: a novel member of the Bol-2 family that promotes apoptosis.";
EMBO J. 17:384-395(1998).
-!- FUNCTION: INDUCES APOPTOSIS. THE ISOFORMS VARY IN CYTOTOXICITY
WITH ISOFORM BIMS BEING THE MOST POTENT AND ISOFORM BIMEL BEING
   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
   054918; 054919; 054919; 054920; 0549218; 054919; 054920; 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEBE-2003 (Rel. 41, Last annotation update)
BCL2-like protein 11 (BCL2 interacting mediator of cell death).
                               0;
   DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
  SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
MEDLINE-98094360; PubMed-9430630;
  CYTOTOXICITY. SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
                                  Indels
  BH3.
Missing (in isoform BimL).
   /FTId=VSP_000536.
Missing (in isoform BimS).
   FTId=VSP_000537.
531C176E5F1AC9AA CRC64;
                               0;
   Pred. No. 9e-05;
  196 AA.
                                  Mismatches
  PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Alternative splicing; Membrane.
  IsoId=054918-2; Sequence=VSP_000536;
  IsoId=054918-1; Sequence=Displayed;
  PRT;
                            .
0
  EMBL; AF032459; AAC40029.1; -.
EMBL; AF032460; AAC40030.1; -.
EMBL; AF032461; AAC40031.1; -.
  22066 MW;
   MGD; MGI:1197519; BC12111.
InterPro; IPR000712; BC12_BH.
100.0%;
   1 QRYGRELRRMSDEF 14
                                     14; Conservative
  STANDARD;
  97
  127
   THE LEAST POTENT.
   Best Local Similarity
  196 AA;
  NCBI_TaxID=10090;
  42
  42
  Name=BimEL;
  Name=BimL;
  Name=BimS;
  BIM_MOUSE
   SEQUENCE
  VARSPLIC
  VARSPLIC
                                  Matches
  SOURCE STANTANT STANT
  δž
   q
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  ;
  Chen D., Simon R.P., Chen J.;

"Cloning of rat binEL and bimL, and their differential expression in ischemia and normal rat brain."

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: INDUCES APOPTOSIS.

-!- SUBGNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, 2 BCL-XL, BFL-1, AND BHER-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
  Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
  Gaps
  Comment=2 isoforms, BOD-L (shown here) and BOD-S, are produced by alternative initiation at Met-1 and Met-104;
   -!- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES
  Hsu S.Y., Lin P., Hsueh A.J.W.; "BOD (BG1-2-related ovarian death gene) is an ovarian BH3 domain-containing proapoptotic Bc1-2 protein capable of dimerization with diverse antiapoptotic Bc1-2 members."
  Note=Isoform BOD-S is produced by alternative initation at Met-104 of isoform BOD-L;
  .;
0
   088498; 088497; Q9WUI8;

16-COT-2001 (Rel. 40, Created)

16-COT-2001 (Rel. 40, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

16-SEP-2003 (Rel. 42, Last annotation update)
   SUBUNIT, AND TISSUE SPECIFICITY
   TISSUE SPECIFICITY: Widely expressed.

DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
Score 42; DB 1; Length 196; Pred. No. 8.7;
  SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
  Indels
  .
m
   Event=Alternative splicing; Named isoforms=3;
   196 AA.
   IsoId=088498-3; Sequence=VSP_000539;
Event=Alternative initiation;
  2; Mismatches
   IsoId=088498-2; Sequence=VSP_000538;
  IsoId=088498-1; Sequence=Displayed;
   or send an email to license@isb-sib.ch).
  PRT;
   Mol. Endocrinol. 12:1432-1440(1998).
   SEQUENCE FROM N.A. (ISOFORM BIML).
   MEDLINE=98400436; PubMed=9731710;
  SEQUENCE FROM N.A., FUNCTION, SUB (ISOFORMS BOD-L; BOD-M AND BOD-S)
  EMBL; AF065433; AAC23595.1; -.
50.6%;
   | :||||: |||
145 RIAQELRRIGDEF 157
   2 RYGRELRRMSDEF 14
   (BY SIMILARITY).
ALTERNATIVE PRODUCTS:
  8; Conservative
  STANDARD;
  NCBI_TaxID=10116;
  CYTOTOXICITY.
  Name-BOD-M;
   BAX OR BAK
  Name=BOD-L
  Name=BimL;
   TISSUE=Ovary
```

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METAL
SEQUENCE
  proteins
  Query Match
   Proc.
METAL
METAL
   HT2A_HUMAN
  RESULT 7
   FT
FT
SO
  0;
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   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   EMBL outstation -
  Usage by and for commercial
   between the Swiss Institute of Bioinformatics and the PMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commen
   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takauchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
   Gaps
   --- CATALYTIC ACTIVITY: Homogentisate + O(2) = 4-maleylacetoacetate.

--- CORACTOR: Iron (BY similarity).

--- PATHWAY: Catabolism of tyrosine; third step.

--- PATHWAY: Catabolism of phenylalanine; fourth step.

--- SIMILARITY: Belongs to the homogentisate dioxygenase family.
   Apoptosis; Alternative splicing; Membrane; Alternative initiation.
CHAIN 1 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-L.
CHAIN 104 196 BCL2-LIKE PROTEIN 11, ISOFORM BOD-S.
  0;
  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homogentisate 1.2-dioxygenase (EC 1.13.11.5) (Homogentisates)
(Homogentisate oxygenase) (Homogentisic acid oxidase).
   TIGRFAMS; TIGROIOIS; hmgA; 1.
Oxidoreductase; Dioxygenase; Phenylalanine catabolism;
Tyrosine catabolism; Metal-binding; Iron; Complete proteome.
  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium,
  -> D (IN REF. 1; AAC23594).
B4D2146F9C0B37A0 CRC64;
  Score 42; DB 1; Length 196;
   Missing (in isoform BOD-M). /FIId=VSP_000539.
  3; Indels
   Missing (in isoform BimL). /FTId=VSP_000538.
   FOR ISOFORM BOD-S.
  457 AA.
  2; Mismatches
   Pred. No.
  Rhizobium loti (Mesorhizobium loti).
   MEDLINE=21082930; PubMed=11214968;
  PS01259; BH3; FALSE_NEG.
       EMBL, AF065432; AAC23594.1; -
EMBL, AF136927; AAC25594.1; -
InterPro; IPR000712; Bc12_BH.
   EMBL; AP003013; BAB53887.1; -.
   22055 MW;
   50.6%;
61.5%;
  IPR005708; HmgA.
  | :||||: |||
|145 RIAQELRRIGDEF 157
   2 RYGRELRRMSDEF 14
   7:331-338(2000).
  8; Conservative
   STANDARD;
   196
196
104
160
97
  127
   Pfam; PF04209; HgmA;
  196 AA;
   Best Local Similarity
  SEQUENCE FROM N.A.
   STRAIN-MAFF303099;
   104
104
146
42
   HMGA OR MLR8303.
  42
  NCBI_TaxID=381;
   HGD_RHILO
   DOMAIN
VARSPLIC
  InterPro;
  INIT_MET
  VARSPLIC
   SEQUENCE
  Query Match
  CONFLICT
  PROSITE;
   Matches
   DNA
   ACO REPETE ELECTE
  δğ
  a
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6
   WEDINE-2588257; Pubbede-12477932; Strouse L.H., Derge J.G., Strousberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strousberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strousberg R.L., Feingold E.A., Grouse L.H., Schemmen C.M., Schuler G.D., Ralschens R.F., Jordan H., More T., Max S.I., Wang J., Habeh N.K., Hobkins R.F., Jordan H., Max Dearner A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rah Esak S.S., Incyuellano N.A., Pothiyuki S., Carninci P., Prange C., Romas S.S., Incyuellano N.A., Pothiyuki S., Carninci P., Prange C., Abramson R.D., Mullahy S.J., Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., An Fahey J., Helton E., Ketteman M., Madan A., Rodigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevohenko Y., Boutfard G.G., Buterfield Y.S.N., Krzywinski M.J., Salaska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schert J. R., Generation and initial analysis of more than 15,000 full-length
  HT2A_HUMAN STANDARD; PRT; 653 AA. (13049; 09N0PB; Cleated) (13049; 09N0PB; Cleated) (1.NOV-1997 (Rel. 35, Created) (28-FRB-2003 (Rel. 41, Last sequence update) (15-SBP-2003 (Rel. 42, Last annotation update) (Rel. 42, Last annotation update) (Interacting protein HT2A (72 kDa Tat-interacting protein) (Tripartite motif-containing protein 32).
   C. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL ACTIVITY OF THE HIV-1 TAT PROTEIN IN VIVO. BINDS SPECIFICALLY TO THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE HIV-2 AND EIAV TAT PROTEINS IN VIVO.

TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY, INTESTINE AND COLON.
   Gaps
  SEQUENCE FROM N.A. MEDINRE-95297135; PubMed-7778269; Fridell R.A., Harding L.S., Bogerd H.P., Cullen B.R.; "Identification of a novel human zinc finger protein that specifically interacts with the activation domain of lentiviral Tat
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   0;
  1; Length 457;
  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
  Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
   IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
6A20B69E9A2B2BD1 CRC64;
   -!- SIMILARITY: Contains 1 RING-type zinc finger.
  DB
   Mismatches
   50.6%; Score 42; 46.7%; Préd. No.
  human and mouse cDNA sequences.";
   2;
   51046 MW;
  425 RYGAELETRODNYID 439
   2 RYGRELRRMSDEFVD 16
  Virology 209:347-357(1995).
   Conservative
351
357
387
457 AA;
  Best Local Similarity Matches 7; Conserv
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
   TRIM32 OR HT2A
  TISSUE=Skin;
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GCR3_YEAST
   Matches
   RESULT 9
   PALD DATE OF SERVICE O
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  ó
   of the ARO4 gene encoding a second DAHP synthase.";

Curr. Genet. 29:441-445[1996].

-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)

AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
   PARTIAL SEQUENCE FROM N.A.
MEDILINE-5620468; PubMed-8625423;
MEDELINE-5620468; LLYY G.P.:
"Aromatic amino-acid biosynthesis in Candida albicans: identification
   Gaps
  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
(EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP
synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
  Eukaryota, Fungi; Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
  ·.
   co-activator activity; TAS.
  DB 1; Length 653; 30;
  4; Indels
  STRAIN=ATCC 11651 / B792;
Sousa S., Pereira S.A., Livi G.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
  -> I (IN REF. 1).
D83B1595CA8378FD CRC64;
  Score 42; DB 1
Pred. No. 30;
1; Mismatches
  370 AA.
   RING-TYPE.
B BOX-TYPE.
F -> I (IN F
   POLY-ALA
  PRT;
  GENEW, HGNC:16880; TRM32.

MIM; 602200; -
607 GG:0005654; C:nucleus; TAS.
GG: GG:0005713; F:transcription co
InterPro; IPR001258; NHL.
InterPro; IPR001315; Znf_Bbox.
InterPro; IPR001841; Znf_Ebox.
InterPro; IPR001841; Znf_ING.
Fam; PF00443; Zf-B_box; 1.
Fam; PF00643; Zf-B_box; 1.
SWART; SW00184; RING; 1.
SWART; SW00184; RING; 1.
FROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS50119; ZF_BBOX; 1.
PROSITE; PS50119; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Znnc-finger; Nuclear protein.
  EMBL; AL133284; CAB92723.1; -. EMBL; BC003154; AAH03154.1; -. HSSP; P29590; 1BOR.
   653 AA; 71988 MW;
   EMBL; U18543; AAA86474.1; -.
  50.6%;
61.5%;
   186 QEYGHEERRVQDE 198
  Ouery Match
Best Local Similarity 61.52
8, Conservative
  1 ORYGRELRRMSDE 13
   Candida albicans (Yeast).
  STANDARD;
  133
   SEQUENCE FROM N.A.
  NCBI_TaxID=5476;
  20
103
27
  AROG_CANAL
ID AROG_CANAL
   SEQUENCE
  CONFLICT
   ZN_FING
   DOMAIN
  RESULT 8
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  ..
O
  Gaps
  Bowman S., Churcher C.M., Badoock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
  οţ
  PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
   01-FEB-1994 (Rel. 28, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last sequence update)
CCR3 protein (ST01 protein) (SUT1 protein)
GCR3 protein (ST01 protein) (SUT1 protein)
GCR3 protein (ST01 or ST1) OR YMR1230 OR YMS564.07 OR YM9553.01.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
   SEQUENCE FROM N.A.
MEDLINE-92380925; PubMed=1512188;
UGMMIRA H., Jigami Y.;
"GGR3 encodes an acidic protein that is required for expression allycolytic genes in Saccharomyces cerevisiae.";
J. Bacteriol. 174:5526-5532(1992).
  6
ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate
  phosphate + phosphate = phosphoenolpyruvate + D-erythrose phosphate + H(2)0.
   ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY)
   -:- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
  Interpro; IPR006219; AroFGH.
Interpro; IPR006218; DAHP1/KDSA.
Pfam; PP00793; DAHP2-87nth_1; 1.
ProDom; PD005060; AroFGH; 1.
TIGRRAMS; TIGR00034; aroFGH; 1.
Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 40291 MW; 11E5E324C8D7B6DB CRC64;
  DB 1; Length 370;
  Indels
  Pandit S., Sternglanz R.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
  Guo Z., Russo P., Sherman F.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
   Saccharomycetales; Saccharomycetaceae; Saccharomyces
   861 AA.
  5; Mismatches
   Pred. No. 24;
   Score 41;
   PRT;
  Ouery Match 49.4%;
Best Local Similarity 42.9%;
   EMBL; U53216; AAB48240.1; -.
   77 YGKRLKKLADELKD 90
   3 YGRELRRMSDEFVD 16
  6; Conservative
   STANDARD;
  SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Pubmed=9169872;
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCBI_TaxID=4932;
  HSSP; P00886;
  GCR3_YEAST
P34160;
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us-09-544-664-29.rsp

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   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   Redpath M. Carrall N., Webb H., Courel M., Amorim A.,
Sedpath M., Carrall N., Webb H., Courel M., Amorim A.,
Cardosodealmeida M.L., Carrington M.;
Submitted (UUL-1997) to the BMEL/Genbank/DDBJ databases.
SUDMILE (UUL-1997) to the BMEL/Genbank/DDBJ databases.
SOLUBLE VARIANT SURFACE GIYCOPROTEIN CONTAINING PHOSPHOINOSITOL
FROM THE CELL WALL OF TRRUEEL PAFER CELL LYSTS. IT ALSO CLENYES
SIMILAR MEMBRANE ANGLES ON SOME MAMMALIAN PROTEINS. VSG LIPASE
MATFICAL ARALY OF SIMILARITY).
-!- CATALYTIC ACTIVITY: Variant-surface-glycoprotein 1,2-didecanoyl-
sn-phosphatidylinositol + H(2)0 = 1,2-didecanoyldlycerol + soluble
variant surface-glycoprotein.
  -:- SUBUNIT: Monomer (By similarity).
-:- SUBCHILDLAR LOCATION: Membrane-associated.
-:- SIMCLIARITY: DOMAIN IS CONSENUED IN DIFFERENT FORMS OF PLC AND IS ESSENTIAL FOR CATALYTIC ACTIVITY.
   Gaps
  Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Variant-surface-glycoprotein phospholipase C (EC 3.1.4.47) (VSG lipase) (Glycosylphosphatidylinositol-specific phospholipase C) (GRC 3.1.4.47)
   .;
0
   Ecocene; EG12972; ygfG.
InterPro; IPR001753; EnCoA_hydrtse.
Prfam; PP00378; ECH; 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
Hypotherical protein; Lyase; Complete proteome; 3D-structure.
SEQUENCE 261 AA; 29172 MW; B6A8A13EC2C2EBE0 CRC64;
  Score 40; DB 1; Length 261;
Pred. No. 25;
   4; Indels
  380 AA
   3; Mismatches
   EMBL, AJ000079; CAA03904.1; -.
Interpro; IPR00909; PI_PLC_Xdom.
Interpro; IPR003633; Varsurfglyc_PPLC.
   EMBL; U28377; AAA69086.1; ALT_INIT.
EMBL; AE000375; AAC75956.1; ALT_INIT.
  PRT;
   48.2%;
   50.0%;
  Pfam; PF00388; PI-PLC-X; 1.
  3 YGRELRRMSDEFVD 16
   21 YGRKLNALSKVFID 34
   7; Conservative
  STANDARD;
  PDB; 1EF8; 24-MAY-00.
PDB; 1EF9; 24-MAY-00.
  Query Match
Best Local Similarity
  SEQUENCE FROM N.A.
  Trypanosoma cruzi.
   NCBI_TaxID=5693;
  PHLC_TRYCR
  PHLC_TRYCR
   Matches
  RESULT 11
ğ
   g
  DEPTHEND ON NEW PRESENCE OF THE PROPERTY OF TH
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   ô
   SHOWN FROM POSITION 708
   NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
   Gaps
   "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
   SEQUENCE FROM N.A.
STRALIF-XI2 / MG1655;
STRALIF-XI2 / MG1655;
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
   ó;
                       Nature 387:90-93(1997).

-!- FUNCTION: REQUIRED FOR EXPRESSION OF GLYCOLYTIC GENES. FOR TRANSCRIPTIONAL ACTIVATOR.

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- SIMILARITY: SOME, TO HUMAN CBEBG.

-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSONWARD AND IS SHORTER (725 AA) DUE TO A FRAMESHIFT.
   DB 1, Length 861;
58;
   Indels
  17. Nuclear protein.

22 30 ASP/GLU-RICH (ACIDIC).

802 825 ARS/ING-RICH (ACIDIC).

804 825 ARS/ING-RICH (BASIC).

164 164 D -> V (IN REF. 3).

633 633 R -> I (IN REF. 3).

704 704 A -> R (IN REF. 3).

861 AA; 100017 WW; EDD04907BDC9207D CRC64;
   PIR: A44919, A44919.
SGD; S0004732; STO1.
GC); GC:0000243; C:Commitment complex; IPI.
GC); GC:0005846; C:SGRNA cap binding complex; IDA.
GC); GC:0003729; F:MRNA binding activity; IPI.
GC); GC:0006371; P:MRNA splicing; IPI.
  P52045, P76643,
P52045, P76643,
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
  Score 41; DB 1
Pred. No. 58;
5; Mismatches
   EMBL; D10224; BAA01076.1; ALT_SEQ.
EMBL; L07650; -; NOT_ANNORATED_CDS.
BMBL; L27744; -; NOT_ANNORATED_CDS.
EMBL; 249273; CAA98274.1; -.
EMBL; 248622; CAA88550.1; -.
  InterPro; IPR003890; IF_EIF4G.
Pfam; PF02854; MIF4G; 1.
SMART; SM00543; MIF4G; 1.
DNA-binding; Nuclear protein.
   :|| | | ::|:|
821 RRYSHEYRELADKFI 835
  49.48;
   40.0%;
   1 ORYGRELRRMSDEFV 15
   Conservative
  Local Similarity
nes 6; Conserv
   Hypothetical proterror YGFG OR B2919. Escherichia coli.
   NCBI_TaxID=562;
   CONFLICT
  Query Match
   SEQUENCE
   DOMAIN
  DOMAIN
  DOMAIN
  Best Loca
Matches
  YGFG_ECOLI
  RESULT 10
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631 AA.

PRT;

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   [2]
SEQUENCE FROM N.A.
STRAIN-ARCG 35210 / B31:
NEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Eraser C.M., Casjens S., Huang W.M., Dodson R., Hickey E.K., Gwinn M.,
Lathigra R., Whiter O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
Peterson J., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Banith H.O., Vanter J.C.;
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Fill C., Cotton M.D., Horst K., Fill C.,  Pan M., Yeh J., Tsai C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE SIGNA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE MAN POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
   Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
   Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
   Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi."; Nature 390:580-586(1997).
  -!- SIMILARITY: Belongs to the sigma-70 factor family.
   Thesis (1994), National Taiwan University, Taiwan.
   01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
  RNA polymerase sigma factor rpoD (Sigma-70).
RPOD OR BB0712.
  Pfam; PF03979; sigma70_r1_1; 1.
Pfam; PF00140; sigma70_r1_2; 1.
Pfam; PF04542; sigma70_r2; 1.
Pfam; PF04545; sigma70_r3; 1.
Pfam; PF04545; sigma70_r4; 1.
PROSITE; PS00715; SIGMA70_1; 1.
   DNA-bindîng; Complete proteome.
DOMAIN 419 432 PO:
  InterPro; IPR000943; Sigma_70.
  EMBL; U17591; AAC44104.1; -. EMBL; AE001171; AAC67061.1; -. EMBL; U68006; AAC45100.1; -. PIR; G70188; G70188.
  SEQUENCE OF 165-614 FROM N.A.
  SEQUENCE OF 89-631 FROM N.A.
STRAIN=ATCC 35210 / B31;
129 GRDLARLVREFVD 141
   STANDARD;
  HSSP; P00579; 1SIG.
TIGR; BB0712; -.
   NCBI_TaxID=139;
   BACTERIA.
   01-0CT-1996 (
   RPSD_BORBU
P52323;
   STRAIN=297
  RESULT 13
RPSD_BORBU
  SOLUTION OF THE WAY WAS A STANDAY OF THE STANDAY OF THE WAY WAS A STAND
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  ó
  RY SEQUENCE FROM N.A.

RY ALS. "Y. Xiao J.P." Ettwiller L., Holden M., Aliotta J., Poh C.L.,
RA VI S. "Y. Xiao J.P." Ettwiller L., Holden M., Aliotta J., Poh C.L.,
RA VI S. "Y. Xiao J.P." Ettwiller L., Holden M., Aliotta J., Poh C.L.,
RA Mare J., Slatko B., Benner J. II;
RA Folion M., Repression of the Apall, NSPI, NSPII, Sapil S.

RY "Cloning and expression of the Apall, NSPI, NSPII, Sapil saci, Scal, and
RY Sapi restriction-modification systems in Escherichia Coli.";

Nol. Gen. Genet. 260:226-231(1998).

RY MOI. Gen. Genet. 260:226-231(1998).

RY Sapi restriction-modification systems in Escherichia Coli.";

Nol. Gen. Genet. 260:226-231(1998).

C. FROTECTS THE DNA FROM CLEAVAGE BY THE APALL ENDONUCLEASE.

C. CTGCAC, CAUSES SPECIFIC METHICARITON ON C.? ON BOTH STRANDS, AND
ROTECTS THE DNA FROM CLEAVAGE BY THE APALL ENDONUCLEASE.

C. GTGCAC, CAUSES SPECIFIC METHICATION ON C.? ON BOTH STRANDS, AND
ROTECTS THE DNA FROM CLEAVAGE BY THE APALL ENDONUCLEASE.

C. GTGCAC, CAUSES SPECIFIC METHICATION ON C.? ON BOTH STRANDS, AND
RY AND C. SIMILARITY: BELONGS TO THE C5-METHILTRANSFERASE FAMILY.
   0;
  Gaps
   Gaps
   Acetobacter pasteurianus (Acetobacter turbidans).
Bacteria: Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Acetobacter.
NCBL_TaxID-438;
  ..
0
   ;
0
  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Modification methylase Apalı (EC 2.1.1.73) (Cytosine-specific methyltransferase Apalı) (M.Apalı).
  48.2%; Score 40; DB 1; Length 429;
  Length 380;
  3; Indels
   Indels
   E011C7D15B33F5F3 CRC64;
  DOMAIN 31 205 DOMAIN X. SEQUENCE 380 AA; 42736 MM; 273CD402552068C5 CRC64;
   PRINTS; FUCKOOSTS; dcm; 1.
TIGRPAMS; TIGROOSTS; dcm; 1.
PROSTIE; PSOMOOS4; CS_WIASE_1; FALSE_NEG.
Transferase; Methyltransferase; Restriction system.

81 BY SIMILARITY: R
   3;
   Score 40; DB 1;
Pred. No. 36;
4; Mismatches 3
  429 AA.
   2; Mismatches
  Pred. No. 41;
Pfam; PF03490; Varsurf_PPLC; 1.
ProDom; PD041675; Varsurfg1yc_PPLC; 1.
SWRT: SW00148; PLCXc; 1.
PROSITE; PSS0007; PIPLC_X_DOMAIN; 1.
  PRT;
  REBASE, 3281, M.Apall.
InterPro; IPROGUISS; CS_DNA_meth.
Plan; PROGUIS5; DNA_methilses; 1.
PRINTS; PROGUIO5; CSMETTRFRASE.
   4;
   EMBL; AF044847; AAC97180.1; -.
   429 AA; 46547 MW;
   48.2%;
   61.5%;
   :: ||| |:|| |:
165 KFFRELDRLSDRFI 178
  2 RYGRELRRMSDEFV 15
  8; Conservative
  Query Match
Best Local Similarity 50.0
Matches 7; Conservative
  STANDARD;
   Hydrolase; Membrane
   Best Local Similarity
  MTA1_ACEPA
  ACT_SITE
SEQUENCE
  Query Match
   RESULT 12
MTA1_ACEPA
   Matches
  δă
   g
```

POLYMERASE CORE BINDING (POTENTIAL).

508 H-T-H MOTIF (BY SIMILARITY). 73642 MW; BD565AB7D8F44796 CRC64;

608

631 AA;

DNA\_BIND SEQUENCE

4 GRELRRMSDEFVD 16

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= = = =

g

Query Match

ŏ ద 6PGL\_THEMA

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MEDILIDE=21848401; PubMed=11859360;

WEDILIDE=21848401; PubMed=11859360;

WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sqouros J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,

Brooks K., Brown D., Erown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Caroin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Caroin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Caroin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Harris D., Hiddell T., Fraser A.,

Holroyd S., Hornsby T., Howarth S., Hauris E., Janckle E.J., Hunt S., Jagels K.,

A Jones L., Jones M., Leather S., McDonald S., McLean J.,

Money P., Moule S., Mangall K., Mulblett D., Odell C.,

A Oliver K., O'Weil S., Pearson D., Quall M.A., Rabbinowitsch E.,

A Laylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rutherford K., Futter C., Aguares S., Stevens K.,

Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Roddward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Woestl D., Hilbert H.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Woestl D., Hilbert H.,

Raber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Lucas M., Rochet W., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rochet W., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

R. Shpakovski G.V., Ussery D., Barrell B. G., Nurse P.,

R. The genome sequence of Schizosaccharomyces pombe.";
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  Jang Y.K., Jin Y.H., Kim B.M., Hong S.H., Fabre F., Park S.D.; (Cloning and sequence analysis of rhp51+, a Schizosaccharomyces pombe homolog of the Saccharomyces cerevisiae RAD51 gene."; Gene 142:207-211(1994).
  Nature 415:871-880(2002).
-i- FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR THE REPAIR OF
  Muris D.F.R., Vreeken K., Carr A.M., Broughton B.C., Lehmann A.R., Lohman P.H.M., Pastink A.;
  SEQUENCE FROM N.A. MEDLINE-93364417; PubMed-8358431; MEDLINE-93364417; PubMed-8358431; Ablionbara A., Ogawa H., Matsuda Y., Ushio N., Ikeo K., Ogawa T. Cloning of human, mouse and fission yeast recombination genes homologous to RAD51 and recA."; Mat. Genet. 4:239-243(1993).
   "Cloning the RAD51 homologue of Schizosaccharomyces pombe.";
Nucleic Acids Res. 21:4586-4591(1993).
  -!- SIMILARITY: BELONGS TO THE RECA FAMILY. RAD51 SUBFAMILY
   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
DNA repair protein rhp51 (RAD51 homolog).
RHP51 OR RAD51 OR SPAC644.14C.
   Schizosaccharomyces pombe (Fission yeast).
   SEQUENCE FROM N.A.
MEDLINE=94252568; PubMed=8194753;
  SEQUENCE FROM N.A.
MEDLINE=94051565; PubMed=8233794;
  DNA DAMAGE CAUSED BY X-RAYS.
  Schizosaccharomyces.
NCBL_TaxID=4896;
  SEQUENCE FROM N.A.
   STRAIN=972;
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   .;
0
   0
  Nelson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-:- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
  Gaps
   phospho-D-gluconate.
-!- PAIHWAY: Pentose phosphate pathway; second step.
-!- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
  Gaps
   -!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-
  Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
  0;
   .;
0
   ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
  47.0%; Score 39; DB 1; Length 220;
                     Length 631;
   3; Indels
   4; Indels
  Hydrolase; Complete proteome.
SEQUENCE 220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;
   28-FEB-2003 (Rel. 39, Last Sequence update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
7hermotoga maritin
                        DB 1;
   365 AA.
   220 AA
  Pred. No. 30;
5; Mismatches
  3; Mismatches
   61;
                        Score 40;
Pred. No. 6
   InterPro; IPR006148; Gluc_gal_isom.
InterPro; IPR005900; Phosphogluconlac.
  PRT;
   PRT;
   Pfam; PF01182; Glucosamine_iso; 1.
TIGRFAMS; TIGR01198; pg1; 1.
   STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
  EMBL; AE001772; AAD36230.1; -.
                     48.2%;
  42.9%;
  ::| ||:| :|:|
EKYEREIRSATDQF 126
  279 YQEELRIFSDDYID 292
  1 QRYGRELRRMSDEF 14
  3 YGRELRRMSDEFVD 16
   Best Local Similarity 50.09
Matches 7; Conservative
  Local Similarity 42.9
les 6; Conservative
   STANDARD;
   STANDARD;
   PHOSPHOGLUCONATE
   PIR; F72289; F72289.
   SEQUENCE FROM N.A.
  NCBI_TaxID=2336;
   TIGE: TM1154;
   RA51_SCHPO
   6PGL_THEMA
```

113

RA51\_SCHPO ID RA51\_S

RESULT 15

Query Match

Matches

δ ద

```
DR EMEL; 222691; CAA808399.1; -.

DR EMEL; 224756; CAA80879.1; -.

DR GeoreDE_Sponde; SPAC644.14c; -.

DR InterPro; IPR003459; HhH.

DR InterPro; IPR001539; RecA.

DR InterPro; IPR001539; RecA.

DR InterPro; IPR001539; RecA.

DR PROSITE; P8000329; RecA.

DR PROSITE; P8000329; RecA.

DR PROSITE; P850162; RECA.

DR PROSITE; P850162; RECA.

DR PROSITE; P850163; RECA.

DR PRO
```

Search completed: September 15, 2003, 17:23:01 Job time : 4.77143 secs

2 RYGRELRRMSDEF 14 |: | |:||:||| 269 RFMRTLQRLADEF 281

QZ Dp

```
09119 staphylococ 099t18 staphylococ 08683 staphylococ 088400 methanopyru 089463 brucella me 089408 brucella su 098xc5 streptomyce 09509 schizosacch 08509 schizosacch 089400 potato mop-081313 homo sapien p78313 homo sapien
  P78313 homo sapien
P78311 homo sapien
P78312 homo sapien
Q9hmu7 halobacteri
Q97819 streptococc
   Q8puzl methanosarc
Q8xd14 escherichia
O64692 arabidopsis
Q910h8 pseudomonas
Q9ficl arabidopsis
Q9a311 caulobacter
   ö
   pyrobaculum
  pyrococcus
   burkholderi
                 Q9v7y6 drosophila Q960b3 drosophila
   SEQUENCE FROM N.A.
MEDLINE-20373792; PubMed=10917738;
Inchara N., Nunez G.;
"Genes with homology to mammalian apoptosis regulators identified in
zebrafish.";
   Gaps
   Bad.
BAD.
BAD.
Brandydanio rerio (Zebrafish) (Danio rerio).
Brandydanio rerio (Zebrafish) (Danio rerio).
Brandydanio rerio (Zebrafish) (Panio rerio).
Brandyderydii. Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OCBL_TaxID-7955;
   ö
  08ztil
  09uzd0
  Length 146;
   Indels
  Cell Death Differ. 7:509-510(2000).

EMBL; AF231017; AAF66962.2; -.

EXRB; DEDGRAY 1G5J.

ERIN; EDB-GRAY-000616-1; bad.

SEQUENCE 146 AA; 16546 MW; 28A56S0BB5107ECB CRC64;
  Last sequence update)
Last annotation update)
  Score 59; DB 13;
Pred. No. 0.047;
   458 AA.
  146 AA
   4; Mismatches
  ALIGNMENTS
P71029
Q9V7Y6
Q9V7Y6
Q95181
Q95181
Q8C83
Q8C83
Q8C63
Q
   097S19
08DR57
08ZT11
09UZQ0
  Created)
   P78313
P78311
P78312
Q9HMU7
   Q8XD14
O64692
Q9I0H8
Q9FIC1
   PRT;
  71.1%;
71.4%;
  13,
   1 QRYGRELRRMSDEF 14
   10; Conservative
   PRELIMINARY;
   1303
2381
7922
11224
1265
109
109
1113
1113
255
255
255
3361
411
   PRELIMINARY;
   548
8592
8762
876
876
876
876
876
877
877
   01-OCT-2000 (TrEMBLrel.
   01-DEC-2001 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel.
  Query Match
Best Local Similarity
40.5
40.5
40.5
   000000000000
  Q8SV57;
   Q919N2
  Q8SV57
   0919N2
  RESULT 1
  RESULT 2
   Q8SV57
ID Q8
AC Q8
  Q919N2
   Q\bar{y}
   g
   Q8xxs6 ralstonia s
Q9xht8 deinococcus
Q9x115 streptomyce
Q8g3z1 bifidobacte
Q9hgq pseudomonas
Q81757 arabidopsis
Q8ev78 mycoplasma
   Q9n9n1 leishmania
Q8tj31 methanosarc
Q8rcc4 thermoanaer
Q8m290 drosophila
Q9fq05 atrichum an
   Q9i9n2 brachydanio
  Q8sv57 encephalito
Q8svf8 encephalito
Q8su90 encephalito
  September 15, 2003, 17:17:31; Search time 17.3714 Seconds (without alignments) 237.680 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Description
   830525
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
  Potal number of hits satisfying chosen parameters:
   830525 seqs, 258052604 residues
  summaries
   using sw model
   0919N2
08SV57
08SVF8
08SU90
08XXS6
09RUK9
   Q9HZQ3
Q8L757
Q8EW78
   Q8TJ31
Q8RCC4
  086321
  BLOSUM62
Gapop 10.0 , Gapext 0.5
   sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_nammal:*
sp_mammal:*
  CONSNI
None
   sp_unclassified:*
  1 ORYGRELRRMSDEFVD 16
  sp_virus:*
sp_vertebrate:*
  Minimum Match 0%
Maximum Match 100%
Listing first 45 su
   sp_bacteriap:*
sp_archeap:*
   sp_organelle:*
   Minimum DB seq length: 0
Maximum DB seq length: 200000000
   sp_phage:*
sp_plant:*
sp_rodent:*
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116
116
116
  US-09-544-664-29
83
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12288
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12088
12048
1205
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139
  protein search,
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6... 77... 1111... 114... 15...

Post-processing:

Database :

Perfect score:

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Sequence:

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Scoring table:

Searched:

Query Match 1

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Salanoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genoone sequence of the plant pathogen Ralstonia solanacearum."; Mature 415:497-502(2002)

Nature 415:497-502(2002)

InterPro; IPR003593; AAA_ATPase.
  Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyret P., Brottier P., Wincker P., Delbac F., Brottier P., Wincker P., Welssenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi";
Nature 414:450-453(2001).
EMBI. ALS90450; CAD25913.1; -.
BRID. ALS90450; CAD25913.1; -.
BRID. ALS90400; CAD25913.1; -.
  Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
   55.4%; Score 46; DB 5; Length 641; 46.7%; Pred. No. 34; Live 5; Mismatches 3; Indels
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  2.m.c.)
01.MAR-2002 (TrEMBLrel. 20, Created)
01.MAR-2003 (TrEMBLrel. 20, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable ATP-binding ABC transporter protein.
RSC2037 OR RS03602.
   01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU11_0030.
ECU11_0030.
Encephalitozoon cuniculi.
  Ralstonia solanacearum (Pseudomonas solanacearum).
   230 AA.
   641 AA
   PRT;
   PRT;
  MEDLINE=21681879; PubMed=11823852;
  STRAIN-GB-M1;
MEDLINE-21576510; PubMed=11719806;
  ||||::|| |:::
RYGRDVMRMLDDMIE 217
                                ||||::|| |:::
RYGRDVMRMLDDMIE 46
  2 RYGRELRRMSDEFVD 16
    2 RYGRELRRMSDEFVD 16
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   PRELIMINARY;
   PRELIMINARY;
  Best_Local Similarity
Matches 7; Conserv
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   NCBI_TaxID=6035;
   NCBI_TaxID=305;
   STRAIN-GMI1000;
   STRAIN-GB-M1;
   Genoscope;
  32
  Query Match
  Q8SU90;
   082090
   Q8XXS6
  RESULT 4
Q8SU90
  RESULT 5
  98XX80
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   Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; Saurin W., Gouy M., Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi."; Matture 411:450453(2001).

EMBL: AL590446; Cab.25529.1; -.

Hypothetical protein.

SEQUENCE 458 AA; 51914 MW; 24111BF78D4A534D CRC64;
   Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
   Encephalitozoon cuniculi.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
  Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
   .
0
  "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
Bature 414:450-453(2001).
EMBL; AL590446; CAD25364.1; -.
Hypothetical protein.
SEQUENCE 477 AA; 54039 MW; B5DCF6299724CC96 CRC64;
   .;
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   Query Match 55.4%; Score 46; DB 5; Length 477; Best Local Similarity 46.7%; Pred. No. 25; Matches 7; Conservative 5; Mismatches 3; Indels
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Pred. No. 24;
5; Mismatches 3; Indels
   Genoscope; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
  01-JUN-2002 (TrEMBIrel. 21, Created)
01-JUN-2002 (TrEMBIrel. 21, Last sequence update)
01-OCT-2002 (TrEMBIrel. 22, Last annotation update)
Hypothetical protein ECU06_1680.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein ECU06_0040.
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MEDLINE=21576510; PubMed=11719806;
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  2 RYGRELRRMSDEFVD 16
  |||||:: || |: ::
13 RYGRDVMRMLDDMIE 27
  Local Similarity 46.7 nes 7; Conservative
   PRELIMINARY;
  Encephalitozoon cuniculi.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=6035;
  STRAIN=GB-M1;
01-JUN-2002 (
01-JUN-2002 (
01-OCT-2002 (
  STRAIN=GB-M1
   STRAIN=GB-M1
  ECU06_0040.
   Genoscope;
  Query Match
   Q8SVF8;
   Q8SVF8
   Matches
   RESULT 3
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"The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract."; proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL; AE014794; AAN25398.1; --
Hypothetical protein; Complete protecome.

SEQUENCE 726 AA, 81866 MW; 6BEB86B6IFCBC586 CRC64;
   Gaps
  Gaps
  SEQUENCE FROM N.A. MEDINE-21125565; PubMed=11222601; MEDINE-21125565; PubMed=11222601; Mamwat W., Lee C.K., Kinoshita H., Yamada Y., Nihira T.; "Identification of the varR gene as a transcriptional regulator of virginiamycin S resistance in Streptomyces virginiae.";
   J. Bacteriol. 183:2025-2031(2001).
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
   ;
  0
   Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
  Berger B.,
   53.0%; Score 44; DB 16; Length 726; 60.0%; Pred. No. 85;
   Length 247;
  4; Indels
   2; Indels
  MEDLINE-22294977; PubMed=12381787; Poffell M.A., Karmirantzou M., Snell B., Vilanova D., Ber. Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M. Pridmore R.D., Arigoni F.,
  Transcription regulation.
   Last sequence update)
Last annotation update)
  Last sequence update)
Last annotation update)
       Streptomycineae; Streptomycetaceae; Streptomyces.
   Score 44; DB 2;
Pred. No. 27;
  726 AA.
   1248 AA.
  2; Mismatches
  Pred. No. 27;
5; Mismatches
   Narrowly conserved hypothetical protein
  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last ann
   Created)
   Bifidobacteriaceae; Bifidobacterium
   PRT;
  PRT;
  EMBL, AB046994; BAB32408.1; -. HSSP; P09164; 2TCT.
InterPro; IPR001647; HTH_TetR.
InterPro; IPR004111; TetR_C.
Pfam; PF00440; tetR; 1.
Pfam; PF02999; tetR_C; 1.
   DNA-binding, Transcription, TrasQUENCE 247 AA; 27328 MW;
   | | | ||:||||:|
241 RVGVVYRRLSDEFLD 255
   53.0%;
   60.08;
   01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
  ||:|: | :||::
186 YGKEVGRTADEFLE 199
  2 RYGRELRRMSDEFVD 16
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Best Local Similarity 50.00,
Best Local 7; Conservative
   3 YGRELRRMSDEFVD 16
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  PRINTS; PR00455; HTHTETR.
  PRELIMINARY;
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   01-MAR-2003
01-MAR-2003
  Query Match
   Q9HZQ3
Q9HZQ3;
  Q8G3Z1
  BL1609
  Matches
  RESULT 8
   RESULT 9
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  Gaps
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   STRAIN=R1;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Laft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Marchevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Fraser C.M.,
  .;
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  "Genome sequence of the radioresistant bacterium Deinococcus
  Streptomyces virginiae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Length 564;
  Length 230;
  Deinococcus radiodurans.

Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.

NCBI_TaxID=1299;
  4; Indels
  3; Indels
  Tick; DALSA,,
TICKTON TRO06047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
Pfam; PF00128; alpha_amylase; 1.
Pfam; PF00128; Ammy; 1.
Hydrolase; Complete proteome.
SEQUENCE 564 AA; 63667 MW; BRF50B9B0DFC8D51 CRC64;
  230 AA; 25231 MW; 7C3FDA1E7A19A2A4 CRC64;
   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
61ycosyl hydrolase, family 13.
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Last annotation update)
  Score 45; DB 16;
Pred. No. 17;
1; Mismatches 4;
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   564 AA.
   247 AA.
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ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
  09AJL5;
01-UDN-2001 (TrEMBLrel. 17, Created)
01-UDN-2001 (TREMBLrel. 17, Last sequol-0CT-2002 (TREMBLRel. 22, Last and
InterPro; IPR003439; ABC_transporter.
   PRT;
  PRT;
  Science 286:1571-1577(1999).
EMBL; AE001983; AAF10944.1; -.
HSSP; P21332; 1UOK.
  54.2%;
64.3%;
   | ||:||: || |
283 YVREMRRVIDEFDD 296
   | || ||| |||
168 QEIGRTLRRLVDEF 181
  1 QRYGRELRRMSDEF 14
  3 YGRELRRMSDEFVD 16
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Matches 9, Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
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   PRELIMINARY;
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   radiodurans R1
   TIGR; DR1375;
  09RUK9;
   Q9AJL5
   Q9RUK9
  VarR.
   RESULT 7
   RESULT 6
  Q9RUK9
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Leishmania major.
   STRAIN-Friedlin;
   STRAIN-HF-
  SECUENCE
  L3302.02.
   MYPE3250.
   Query Match
  Q8EW78;
  : IN6N60
  Q8EW78
  U9N9N1
   RESULT 12
  RESULT 11
   [2]
   Q8EW78
   IN6N60
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  STRAIN=AUCC 15692 / PAO1;

STRAIN=AUCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

A Stover C.K., Pham X.-O.T., Ervin A.L., Mizoguchi S.D., Warrener P.,

A Hickey M.J., Brinkman F.S.L., Hufhagle W.O., Kowalik D.J., Lagrou M.,

A Garber R.L., Goltry L., Tolentino E., Westbrock-Wadnan S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Relzer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Roportunistic pathogen";

"Ruture 406:559-964 (2000).

RMEL; AEO04720; AAG06332.1; -.

RMEL; AEO04720; AAG06332.1; -.

RICEPRO: IPRO00408; Reg_chr_condens.

Pfam: PF02514; cobn.Mg_chel, 1.

PROSITE; PS00626; RCC1_2; 1.
   SEQUENCE FROM N.A.

SOUTHWICK A., Nguyen M., Tripp M., Falm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan W.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Torcumi M., Wallender E.K., Wong C.,
Mu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.,
Submitted (JUL-2002) to the EMBL/Genbank/DDBJ databases.
   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
  Gaps
   SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
Strain-cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKI18269; BAC42887.1; -.
  2,
   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
  Length 1248;
  53.0%; Score 44; DB 16; Length 124
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  .1 protein.
205 AA; 22583 MW; 1BD8D1358ECFFF81 CRC64;
  Last sequence update)
Last annotation update)
  205 AA.
   Created)
Cobalamin biosynthetic protein CobN.
COBN OR PA2944.
  PRT;
  : || |:| |:||| |
615 ESYGPLRDLERLADEFYD 632
  1 QRYG--RELRRMSDEFVD 16
   Pseudomonadaceae; Pseudomonas
  01-ocr-2002 (TEMBLES) 22,
01-MAR-2003 (TEMBLES) 23,
HYPOthetical protein.
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   SEQUENCE FROM N.A.
   Complete proteome.
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  SEQUENCE
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   Matches
   RESULT 10
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  Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Soshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
EMBL; APO04171; BAC44118.1; --
Complete protecome.
  Gaps
   Gaps
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
   Bāctēria; Fīrmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
  0;
   0;
  Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,
Quail M., Rajandream M.A., Barrell B.G.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
  STRAIN-Friedlin;

MEDLINE-88146435;
PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1988).
EMBL; AL359781; CAB95305-1;
InterPro; IPR004273; Dynein_heavy.
              DB 10; Length 205; 32;
   Length 804;
   Indels
  3; Indels
  804 AA; 88008 MW; 69C71AA628FEF7A3 CRC64;
  01-OCT-2000 (TrEMBLrel. 15, Created)
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01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Dynein heavy chain, cytosolic.
  01-MAR-2003 (TrEWBLrel. 23, Created)
01-MAR-2003 (TrEWBLrel. 23, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
   51.8%; Score 43; DB 16; Le
66.7%; Pred. No. 1.4e+02;
live. 2; Mismatches 2;
  PRT; 5635 AA.
  804 AA.
  Mismatches
                Score 43;
Pred. No.
  PRT;
   InterPro; IPR000169; Shprot_acsite
   STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
  Cation-transporting p-type ATPase.
              51.8%;
61.5%;
  100 GSQIRRCSSEFVD 112
Query Match
Best Local Similarity 61.5*
  428 GSELREMSDEYL 439
  4 GRELRRMSDEFVD 16
  Best_Local Similarity 66.7
Matches 8; Conservative
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  PRELIMINARY;
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  SEQUENCE FROM N.A.
   NCBI_TaxID=28227;
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Query Match
Best Local Similarity 58.3°
   :: | |:|||:|
170 KQLNRVSDEFMD 181
   8; Conservative
  5 RELRRASDEFVD 16
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   Sest Local Similarity
  [1]
SEQUENCE FROM N.A.
  Complete proteome. SEQUENCE 260 AA;
   ARTI OR TIE0512.
   Query Match
   08MZ90;
   08MZ90
   Matches
   RESULT 15
   Q8MZ90
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   PROJECTE FROW N.A.

SEQUENCE FROW N.A.

SERIN-C2A / ATCC 35395 / DSM 2834;

MEDILINE=1129760; PubMed=11932238;

MEDILINE=1129760; PubMed=11932238;

A allagan J.E., Nusbaum C., Roy A., Emirrov S., Atnoor D., Brown A.,

Ritziugh W., Calvo S., Engel-Thomann N., DeArellano K., Johnson R.,

A llen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

A llen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

A llen N., Naylor J., Stange-Thomann D.E., Graham D.A., Guss A.M.,

Redderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Redderich R., Jarrell K.F., Jung H., Macario A.J.L., Paulsen I.,

Prichett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.E.cin a cetivorans reveals extensive metabolic

and physiological diversity.";

Genome Res. 12:322-42(2002).

RMBL: ABOIL107; AAM07308:1: -

InterPro; IPR003593; AAA_ATPasse.

No Flare Pro; IPR003593; AAA_ATPasse.

No Flare Proportor Proposed Propos
   Gaps
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  01-00N-2002 (TrEMBLrel. 21, Created)
01-5UN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC-type amino acid transport system, periplasmic component.
   51.8%; Score 43; DB 5; Length 5635; 72.7%; Pred. No. 1.1e+03; ative 2; Mismatches 1; Indels
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  1; Indels
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SEOUENCE 5635 AA; 620050 MW; 64A9EB81A9B14641 CRC64;
   Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
  Prodom; roccosts AAA; 1.
SMART; SM00321, AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Complete proteone.
ATP-binding; Complete proteone.
ATP-binding; 23676 MW; B548F93D94D109C9 CRC64;
  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
ABC transporter, ATP-binding protein.
  Score 42; DB 17;
Pred. No. 49;
1; Mismatches 1;
   260 AA.
   213 AA.
                              SMART; SM00382; ÅAA; 4.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
   Pfam: PF00005; ABC_tran; 1.
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Best Local Similarity 72./*;
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   23
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   Q8TJ31
  MA3957
   RESULT 14
Q8RCC4
   RESULT 13
Q8TJ31
   BABARA
   TD DTT DDT TD DD
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   NA DR SO NA 
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  STAIN-MB4 / JCM 11007;
X MEDILINE-1992816; bubmed=11997336;
A Bao Q. Tian Y. Li W. Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
A Chen Y., Xue Y., Lia X., Huang L., Dong X., Ma Y., Ling L.,
A Tan H., Chen R., Wang J., Yu J., Yang H.;
A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
R Embi. ABO13022; ABM3788 1.;
R InterPro: IPR01311; SBP/glu_receptor.
R InterPro: IPR001311; SBP/glu_receptor.
R InterPro: IPR001389; SBP_bac_3.
R Pfan: PF00497; SBP_bac_3.
R Pfan: PF004905; PBPP: 1.
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  Gaps
   SEQUENCE FROM N.A.
StapLeron M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall G.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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   AT26020p.
CG30456 OR CG15612 OR CG15613.
CG30456 OR CG15612 OR CG15613.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
The Machinidae of Company o
   Score 42; DB 16; Length 260;
Pred. No. 61;
4; Mismatches 1; Indels
Thermoanaerobacter tengcongensis.
Bacteria: Firmicutes; Clostridia; Thermoanaerobacteriaceae; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
  50.6%; Score 42; DB 5; Length 297; 53.3%; Pred. No. 70;
  Indels
  Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY113300, AAM29305.1; -.

ENJABSE, PERGUODS04.56; CG304.56.

InterPro; IPR000219; RhoGEF.

PROM: PF00621; RhoGEF.

PROSTE: PS50101; DH.2; 1.

SEQUENCE 297 AA; 35804 MW; S8FDBF3DF688D99A CRC64;
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01-0CT-2002 (TrEMBLrel, 22, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
  3;
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Search completed: September 15, 2003, 17:25:49 Job time : 18.3714 secs

us-09-544-664-29.rspt

us-09-544-664-29.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model - protein search, OM protein

September 15, 2003, 17:18:16 ; Search time 7.2 Seconds (without alignments) 213.708 Million cell updates/sec Run on:

US-09-544-664-29 83 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 QRYGRELRRMSDEFVD 16 Scoring table: Sequence:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_76:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|     |        | Description | bad protein - mous | glycosyl hydrolase | cobalamin biosynth | valine-tRNA ligase | hypothetical cytos | Н     | au    | GCR3 protein - yea | hypothetical prote | conserved hypothet | conserved hypothet | hypothetical prote | probable enzyme [i | enzy  | ical prc |       | hypothetical prote | transcription regu |       | probable Fe-S oxid | transcription init | hypothetical prote | -      | hypothetical prote | hypothetical prote | ij | •   | oxidoreductase, so | transporter homolo |
|-----|--------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------|-------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------|----------|-------|--------------------|--------------------|-------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|----|-----|--------------------|--------------------|
|     |        |             | 567                | 540                | 33278              | 39949              | 53414              | 85356 | 40297 | 44919              | 84388              | 95043              | 97913              | 75088              | 91102              | 85948 | 65076    | 52577 | B83311             | 87644              | 24986 | 97123              | 70188              | 96695              | E87441 | ~                  | AC3365             | m  | 534 | 72289              | 0                  |
|     |        | 7           |                    |                    | 3 68               |                    |                    |       |       |                    |                    |                    |                    |                    |                    |       |          |       |                    |                    |       |                    |                    |                    |        |                    |                    |    | 2 B | ĺ×ι                | O                  |
|     |        | ac a        | '                  |                    |                    |                    |                    |       |       |                    |                    | _                  | ~                  | <u></u>            |                    |       | 10       | 10    |                    | 1                  | m     | 10                 |                    | <u></u>            | m      | -                  | m                  | ~  | 7   | 0                  | ın                 |
|     | 1      | rengru      | 20                 | 26                 | 124                | 87                 | 19                 | 44    | 577   | 85                 | œ                  | 10                 | 11                 | 21                 | 27                 | 27    | 27       | 33    | 36                 | 41                 | 42    | 44                 | 63                 | 513                | 19     | 41                 | 7                  | 17 | 20. | 22                 | 27                 |
| οķο | Query  | Match       | 88.0               | 4.                 | 53.0               | 0.                 |                    | 49.4  | 49.4  | 49.4               | 48.2               | 48.2               | ω,                 | 48.2               | æ                  | œ     | 48.2     | æ     | œ.                 | 48.2               | œ,    | ω.                 | 48.2               |                    | 7.     | 7.                 | ۲.                 |    | 7.  | 47.0               | 47.0               |
|     |        | score       | · /-               | 45                 |                    | 42                 | 41.5               | 41    | 41    | 41                 | 40                 | 40                 | 40                 | 40                 | 40                 | 40    | 40       | 40    | 40                 | 40                 | 40    | 40                 | 40                 | 40                 | 39.5   | σ,                 | 9<br>8             | 38 | გ   | 30                 | 33                 |
|     | Result | Q           | П                  | 2                  | ო                  | 4                  | ស                  | 9     | 7     | 80                 | σn                 | 10                 | 11                 | 12                 | 13                 | 14    | 15       | 16    | 17                 | 18                 | 19    | 20                 | 21                 | 22                 | 23     | 24                 | 25                 | 26 | 27  | 28                 | 29                 |

| DNA repair protein |        | RAD51 protein homo | hypothetical prote | hypothetical prote | sigma 2 protein - | siqma 2 protein - | trigger factor [im | site-specific DNA- | acylaminoacyl-pept | hypothetical profe | valine-tRNA ligase | probable kinesin - | two-component hybr | similar to late em | hypothetical prote |
|--------------------|--------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| E90121             | D86200 | S42107             | T32163             | T31738             | FOXRL2            | FOXR3D            | AB0558             | CIBPRH             | F90299             | T29772             | SYBSVS             | B71405             | AE2452             | T02712             | S64604             |
| 7                  | 7      | 7                  | 7                  | 7                  | Н                 | <del>( </del>     | 7                  | ۲                  | 7                  | 7                  |                    | H                  | ~                  | 7                  | 7                  |
| 331                | 360    | 365                | 380                | 383                | 418               | 418               | 432                | 503                | 536                | 689                | 880                | 959                | 965                | 1805               | 1967               |
| 47.0               | 47.0   | 47.0               | 47.0               | 47.0               | 47.0              | 47.0              | 47.0               | 47.0               | 47.0               | 47.0               | 47.0               | 47.0               | 47.0               | 47.0               | 47.0               |
| <u>გ</u>           | 38     |                    |                    | 39                 |                   |                   |                    |                    |                    |                    |                    |                    |                    | 99                 |                    |
| 30                 | 31     | 32                 | 33                 | 34                 | 35                |                   | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

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Dad protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C;Date: 03-Mar-1995
B;Pang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
R;Pang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Reference number: A55671; MUID:99136361; PMID:7834748
  0
   Gaps
   A)Status: preliminary, not compared with conceptual translation A)Molecule type: mRNA A)
  ö
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  Query Match
```

1 QRYGRELRRMSDEF 14 QΥ

145 QRYGRELRRMSDEF 158 g

RESULT 2

glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000
C;Accession: H75403
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.;
K.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Vanter, J.C.; Fraser, C.M.
S;Sinct S86, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A7550; MUID:20036896; PMID:10567266

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-564 <WHI> A;Cross.references: GB:AE001983; GB:AE000513; NID:g6459123; PIDN:AAF10944.1; PID:g64! A;Experimental source: strain Rl

C; Genetics:

A;Gene: DR1375 A;Map position: 1 C;Superfamily: alpha-glucosidase; alpha-amylase core homology

Gaps 0; Query Match 54.2%; Score 45; DB 2; Length 564; Best Local Similarity 64.3%; Pred. No. 14; Matches 9; Conservative 2; Mismatches 3; Indels

0;

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hypothetical protein A74930490 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Spaces)  κ, μγπε, Μ.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; Duest submitted to the EMBL Data Library, May 1998
A;Reference number: Z21919
A;Accession: 140297
A;Starm......
C;Accession: AD3414
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
i Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the feaultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:1175668
A;Status: preliminary
A;Molecule type: DNA
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  A;Residues: 1-577 <IYN>
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  A; Cross_references: GB: AE008917; PIDN: AAL52479.1; PID:g17983287; GSPDB: GN00190 A; Experimental source: strain 16M C; Genetics:
   A; Cross-references: GB:NC_001268; NID:97269950; PIDN:CAB79767.1; GSPDB:GN00140
  membrane transporter - fission yeast (Schizosaccharomyces pombe)
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C;Accession: T40297
R;Lyne, M; Wood, V; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl.
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  17;
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   A; Molecule type: DNA
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   A;Gene: AT4q30490
  A; Gene: BMEI1298
   A; Map position:
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Matches 11;
   Query Match
   C; Genetics:
  C; Genetics:
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   RESULT 7
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   A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, A/Fitle: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, A/Accession: 683278
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  M.J.; Br
K.; Lim,
   G83278

Cobalamin biosynthetic protein CobN PA2944 [imported] - Pseudomonas aeruginosa (strain cobalamin biosynthetic protein CobN PA2944 [imported] - Pseudomonas aeruginosa (strain c;Species: Pseudomonas aeruginosa (;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Mar-2001 c;Accession: G83278

S;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
   hypothetical cytosolic protein BME11298 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #text_change 01-Feb-2002 C;Date: 01-Feb-2002
   C; Accession: E89949
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
   0;
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A;Cross-references: GB:B&000018; PID:g13701460; PIDN:BAB42754.1; GSPDB:GN00149
A;Experimental source: strain N315
   A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89949
   -2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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61.5%;
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283 YVREMRRVIDEFOD 296
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251 GRELPILADEYVD 263
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Best Local Similarity
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   A; Gene: vals
   Matches
   RESULT 5
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Read, T.D.; Peterson, S.; I non, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp: Science 293, 498-506, 2001
A.hathors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A.fatle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A.Recession: B95043
  conserved hypothetical protein SP0372 [imported] - Streptococcus pneumoniae (strain % C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
  B.S
2, S
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   A;Cross-references: GB:AE005672; PIDN:AAK74539.1; PID:g14971841; GSPDB:GN00164; TIGR
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C;Genetics:
  C, Accession: D97913
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e, R.; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. e, R.; Leblano, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Attle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MuID:21429245; PMID:11544234
A; Accession: D97913
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   A;Cross-references: GB:AE007317; PIDN:AAK99136.1; PID:915457889; GSPDB:GN00174 C;Genetics:
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19;
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  DB 2
18;
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  48.2%;
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   48.2%;
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   Conservative
   2 RYGRELRRMSDE 13
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9; Conserve
  Similarity
8; Conserv
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Best Local Similarity
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Best Local S:
Matches 8;
   A; Gene: SP0372
  RESULT 11
  Matches
  RESULT 12
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  GCR3 protein - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein WMS54.07; protein EM953.01; protein EMR125w
C.Species: Saccharomyces cerevisiae
C.Species: 30-Sep-1993 #sequence_revisiae
C.Date: 30-Sep-1999
C.Species: 30-Sep-199
C
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: F84388
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Proc. Natl. Adam, W.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li. A;Reference number: A84160; MUID:20504483; PMID:11016950
  A Accession: S53055
A; Molecule type: DNA
A; Resaidues: 339-888 DAD
A; Cross-references: EMBL: Z48622; NID: 9728663; PIDN: CAA88550.1; PID: 9728664; MIPS: VMR125N
B; Lye, G.; Churcher, C.M.
Submitted to the EMBL Data Library, May 1995
A; Reference number: S54014
A; Molecule type: DNA
A; References: YMPNRKRG', 6-489 < LYE>
A; Molecule type: DNA
A; Cross-references: WRBL: Z49273; NID: 9809577; PIDN: CAA89274.1; PID: 9809584; MIPS: YMR125N
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  RRYSHEYRELADKFI 832
   40.08;
   A; Map position: 13R
C; Keywords: DNA binding; nucleus
  1 QRYGRELRRMSDEFV 15
                        Similarity 57.1%;
8; Conservative
  :||::||||
FGRKIRRMSKMAVD 576
49.48;
   3 YGRELRRMSDEFVD 16
  Conservative
   Ouery Match
Best Local Similarity
Matches 6; Conserv
   563
   818
Query Match
Best Local 8
  Matches
  δŽ
   qq
  QΫ
  g
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S

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A; Experimental source: strain 0157:H7, substrain EDL933
   Job time : 9.2 secs
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   δy
   qq
  QΫ
  g
hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A7508
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Reference number: A75001
A;Reference second argument argumen
   A;Cross-references: GB:AE005174; NID:g12517451; PIDN:AAG58045.1; GSPDB:GN00145; UWGP:243
  Distribution of the problem of the p
   ·-i
  ö
   A; Residues: 1-275 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB37212.1; PID:g13363261; GSPDB:GN00154
A; Cross-references: GB:BA000007; PIDN:BAB37212.1; PID:g13363261; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: ECs3789
C; Superfamily: naphthoate synthase; encyl-CoA hydratase homology
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   Gaps
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   DB 2; Length 219; 37;
   3; Indels
  Mismatches
   48.2%; Score 40; 47.1%; Pred. No.
  2 RYGRELRRMS -- DEFVD 16
  48.2%;
  3 YGRELRRMSDEFVD 16
  35 YGRKLNALSKVFID 48
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Best Local Similarity 50.0*
  Conservative
   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <STO>
  Best Local Similarity
Matches 8; Conserv
  A; Accession: A85948
  A;Gene: PAB1640
   Query Match
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  g
  임
   δŽ
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hypothetical protein b2919 - Escherichia coli (strain K-12)

C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: F65076
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.G.; Mau, B.; Shao, Y.
  A; Molecule type: DNA
A; Residues: 1-275 <BLAT>
A; Residues: 1-275 <BLAT>
A; Cross-references: GB:AB000375; GB:U00096; NID:91789282; PIDN:AAC75956.1; PID:91789; A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: naphthoate synthase; encyl-coA hydratase homology
F; 40-192/Domain: encyl-coA hydratase homology <BCE>
   ő
   ö
  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
   Gaps
   Gaps
   ó
   .;
0
C;Genetics:
A;Gene: ygfG
C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
  Length 275;
  Length 275;
   A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65076
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   Indels
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46;
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Pred. No. 46;
3; Mismatches
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  3 YGRELRRMSDEFVD 16
  35 YGRKLNALSKVFID 48
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  35 YGRKLNALSKVFID 48
   Query Match
Best Local Similarity 50.0°
Matches 7; Conservative
  Best Local Similarity 50.0 Matches 7; Conservative
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